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(54) Title: SUSCEPTIBILITY GENE FOR MYOCARDIAL INFARCTION; METHODS OF TREATMENT

(57) Abstract: Linkage of myocardial infarction (MI) and a locus on chromosome 13q12 is disclosed. In particular, the FLAP gene within this locus is shown by genetic association analysis to be a susceptibility gene for MI. Pathway targeting for treatment and diagnostic applications in identifying those have MI or at risk of developing MI, in particular are described.

-1-

SUSCEPTIBILITY GENE FOR MYOCARDIAL INFARCTION; METHODS OF TREATMENT

RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 60/449,331, filed on February 21, 2003, and claims the benefit of U.S. Provisional Application No. 60/419,433, filed on October 17, 2002. The entire teachings of the above applications are incorporated herein by reference.

BACKGROUND OF THE INVENTION

Myocardial infarction (MI) and Acute Coronary Syndrome (ACS), *e.g.*, unstable angina, non-ST-elevation myocardial infarction (NSTEMI) or ST-elevation myocardial infarction (STEMI), are the leading causes of hospital admissions in industrialized countries. Cardiovascular disease continues to be the principle cause of death in the United States, Europe and Japan. The costs of the disease are high both in terms of morbidity and mortality, as well as in terms of the financial burden on health care systems.

Myocardial infarction generally occurs when there is an abrupt decrease in coronary blood flow following a thrombotic occlusion of a coronary artery previously damaged by atherosclerosis. In most cases, infarction occurs when an atherosclerotic plaque fissures, ruptures or ulcerates and when conditions favor thrombogenesis. In rare cases, infarction may be due to coronary artery occlusion caused by coronary emboli, congenital abnormalities, coronary spasm, and a wide variety of systemic, particularly inflammatory diseases. Medical risk factors for MI include cigarette smoking, diabetes, hypertension and serum total cholesterol levels > 200 mg/dL, elevated serum LDL cholesterol, and low serum HDL cholesterol. Event rates in individuals without a prior history of cardiovascular disease are about 1%. In individuals who have had a first MI or ACS, the risk of a repeat MI within

the next year is 10-14%, despite maximal medical management including angioplasty and stent placement.

Atherosclerosis can affect vascular beds in many large and medium arteries. Myocardial infarction and unstable angina (acute coronary syndrome (ACS)) stem from coronary artery atherosclerosis, while ischemic stroke most frequently is a consequence of carotid or cerebral artery atherosclerosis. Limb ischemia caused by peripheral arterial occlusive disease (PAOD) may occur as a consequence of iliac, femoral and popliteal artery atherosclerosis. The atherosclerotic diseases remain common despite the wide-spread use of medications that inhibit thrombosis (aspirin) or treat medical risk factors such as elevated cholesterol levels in blood (statins), diabetes, or hypertension (diuretics and anti-hypertensives).

Atherosclerotic disease is initiated by the accumulation of lipids within the artery wall, and in particular, the accumulation of low-density lipoprotein (LDL) cholesterol. The trapped LDL becomes oxidized and internalized by macrophages. This causes the formation of atherosclerotic lesions containing accumulations of cholesterol-engorged macrophages, referred to as "foam cells". As disease progresses, smooth muscle cells proliferate and grow into the artery wall forming a "fibrous cap" of extracellular matrix enclosing a lipid-rich, necrotic core. Present in the arterial walls of most people throughout their lifetimes, fibrous atherosclerotic plaques are relatively stable. Such fibrous lesions cause extensive remodeling of the arterial wall, outwardly displacing the external, elastic membrane, without reduction in luminal diameter or serious impact on delivery of oxygen to the heart. Accordingly, patients can develop large, fibrous atherosclerotic lesions without luminal narrowing until late in the disease process. However, the coronary arterial lumen can become gradually narrowed over time and in some cases compromise blood flow to the heart, especially under high demand states such as exercise. This can result in reversible ischemia causing chest pain relieved by rest called stable angina.

-3-

In contrast to the relative stability of fibrous atherosclerotic lesions, the culprit lesions associated with myocardial infarction and unstable angina (each of which are part of the acute coronary syndrome) are characterized by a thin fibrous cap, a large lipid core, and infiltration of inflammatory cells such as T-lymphocytes and monocyte/macrophages. Non-invasive imaging techniques have shown that most MI's occur at sites with low- or intermediate- grade stenoses, indicating that coronary artery occlusion is due most frequently to rupture of culprit lesions with consequent formation of a thrombus or blood clot and not solely due to luminal narrowing by stenosis. Plaque rupture may be due to erosion or uneven thinning of the fibrous cap, usually at the margins of the lesion where macrophages enter, accumulate, and become activated by a local inflammatory process. Thinning of the fibrous cap may result from degradation of the extracellular matrix by proteases released from activated macrophages. These changes producing plaque instability and risk of MI may be augmented by production of tissue-factor procoagulant and other factors increasing the likelihood of thrombosis.

In acute coronary syndrome, the culprit lesion showing rupture or erosion with local thrombosis typically is treated by angioplasty or by balloon dilation and placement of a stent to maintain luminal patency. Patients experiencing ACS are at high risk for a second coronary event due to the multi-vessel nature of coronary artery disease with event rates approaching 10-14% within 12 months after the first incident.

The emerging view of MI is as an inflammatory disease of the arterial vessel wall on preexisting chronic atherosclerotic lesions, sometimes triggering rupture of culprit lesions and leading to local thrombosis and subsequent myocardial infarction. The process that triggers and sustains arterial wall inflammation leading to plaque instability is unknown, however, it results in the release into the circulation of tumor necrosis factor alpha and interleukin-6. These and other cytokines or biological mediators released from the damaged vessel wall stimulate an inflammatory response in the liver causing elevation in several non-specific general inflammatory markers

including C-reactive protein. Although not specific to atherosclerosis, elevated C-reactive protein (CRP) and serum amyloid A appear to predict risk for MI, perhaps as surrogates for vessel wall inflammation.

Although classical risk factors such as smoking, hyperlipidemia, hypertension, and diabetes are associated with many cases of coronary heart disease (CHD) and MI, many patients do not have involvement of these risk factors. In fact, many patients who exhibit one or more of these risk factors do not develop MI. Family history has long been recognized as one of the major risk factors. Although some of the familial clustering of MI reflects the genetic contribution to the other conventional risk factors, a large number of studies have suggested that there are significant genetic susceptibility factors, beyond those of the known risk factors (Friedlander Y, *et al.*, *Br. Heart J.* 1985; 53:382-7, Shea S. *et al.*, *J. Am. Coll. Cardiol.* 1984; 4:793-801, and Hopkins P.N., *et al.*, *Am. J. Cardiol.* 1988; 62:703-7). Major genetic susceptibility factors have only been identified for the rare Mendelian forms of hyperlipidemia such as a familial hypercholesterolemia.

Genetic risk is conferred by subtle differences in genes among individuals in a population. Genes differ between individuals most frequently due to single nucleotide polymorphisms (SNP), although other variations are also important. SNP are located on average every 1000 base pairs in the human genome. Accordingly, a typical human gene containing 250,000 base pairs may contain 250 different SNP. Only a minor number of SNP are located in exons and alter the amino acid sequence of the protein encoded by the gene. Most SNP have no effect on gene function, while others may alter transcription, splicing, translation, or stability of the mRNA encoded by the gene. Additional genetic polymorphism in the human genome is caused by insertion, deletion, translocation, or inversion of either short or long stretches of DNA. Genetic polymorphisms conferring disease risk may therefore directly alter the amino acid sequence of proteins, may increase the amount of protein produced from the gene, or may decrease the amount of protein produced by the gene.

As genetic polymorphisms conferring risk of disease are uncovered, genetic testing for such risk factors is becoming important for clinical medicine. Examples are apolipoprotein E testing to identify genetic carriers of the apoE4 polymorphism in dementia patients for the differential diagnosis of Alzheimer's disease, and of Factor V Leiden testing for predisposition to deep venous thrombosis. More importantly, in the treatment of cancer, diagnosis of genetic variants in tumor cells is used for the selection of the most appropriate treatment regime for the individual patient. In breast cancer, genetic variation in estrogen receptor expression or heregulin type 2 (Her2) receptor tyrosine kinase expression determine if anti-estrogenic drugs (tamoxifen) or anti-Her2 antibody (Herceptin) will be incorporated into the treatment plan. In chronic myeloid leukemia (CML) diagnosis of the Philadelphia chromosome genetic translocation fusing the genes encoding the Bcr and Abl receptor tyrosine kinases indicates that Gleevec (STI571), a specific inhibitor of the Bcr-Abl kinase should be used for treatment of the cancer. For CML patients with such a genetic alteration, inhibition of the Bcr-Abl kinase leads to rapid elimination of the tumor cells and remission from leukemia.

Many general inflammatory markers predict risk of coronary heart disease, although these markers are not specific to atherosclerosis. For example, Stein (Stein, S., *Am J Cardiol*, 87 (suppl):21A-26A (2001)) discusses the use of any one of the following serum inflammatory markers as surrogates for predicting risk of coronary heart disease including C-reactive protein (CRP), serum amyloid A, fibrinogen, interleukin-6, tissue necrosis factor-alpha, soluble vascular cell adhesion molecules (sVCAM), soluble intervascular adhesion molecules (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9. Elevation in one more of these serum inflammatory markers is not specific to coronary heart disease but also occurs with age or in association with cerebrovascular disease, peripheral vascular disease, non-insulin dependent diabetes, osteoarthritis, bacterial infection, and sepsis.

Serum C-reactive protein (CRP) is viewed as a convenient and sensitive marker of systemic inflammation. Generally CRP is measured in serum samples using commercially available enzyme-linked immunosorbent assays (EIA). Consistent across multiple published studies is the finding of a correlation between increased risk for coronary artery disease with increased serum CRP. For example, in the Women's Health Study, CRP was measured in 27,939 apparently healthy American women. The cut-off points for quintiles of serum CRP in women were: less than or equal to 0.49, more than 0.49 to 1.08, more than 1.08 to 2.09, more than 2.09 to 4.19, and more than 4.19 mg CRP per liter, see Ridker, P.M. *et al.*, *New England. J. Med.*, 347: 1557-1565 (2001). In comparison to the lowest quintile, and even when adjusting for age, every quintile more than 0.49 mg CRP per liter was associated with increased risk for coronary heart disease with the highest relative risk of 4.5 seen for those women in the highest quintile of serum CRP (more than 4.19 mg CRP per liter). A similar correlation between increased serum CRP and increased risk for coronary heart disease in women has been reported (Ridker, P.M. *et al.*, *New Engl. J. Med.*, 342:836-843 (2000) and Bermudez, E.A. *et al.*, *Arterioscler. Thromb. Vasc. Biol.*, 22: 1668-1673 (2002)). Men also show a correlation between increased serum inflammatory markers such as CR and increased risk for coronary heart disease has been reported (Doggen, C.J.M. *et al.*, *J. Internal Med.*, 248:406-414 (2000) and Ridker, P.M. *et al.*, *New England. J. Med.*, 336: 973-979 (1997)). Quintiles for serum CRP as reported by Doggen *et al.*, were less than 0.65, more than 0.65 to 1.18, more than 1.18 to 2.07, more than 2.07 to 4.23, and more than 4.23 mg CRP per liter. Unlike women, elevated serum CRP correlates with increased relative risk for coronary heart disease only in the 4th and 5th quintiles of CRP (relative risk of 1.7x and 1.9x, respectively).

Serum CRP in women also has been measured in conjunction with lipid markers such as levels of serum low density lipoprotein-cholesterol (LDL-C). In the study by Ridker, P.M. *et al.* (2002), serum CRP and LDL-C are minimally correlated, screening for both serum markers provided better

prognostic indication than either alone. Thus, women with serum CRP above median values (more than 1.52 mg CRP per liter) and also serum LDL-C above median values (more than 123.7 mg LDL-C per deciliter) were at highest risk for coronary heart disease.

5 Elevated CRP or other serum inflammatory markers is also prognostic for increased risk of a second myocardial infarct in patients with a previous myocardial infarct (Retterstol, L. *et al.*, *Atheroscler.*, 160: 433-440 (2002)).

10 Since CRP is produced in the liver, there is no a priori mechanistic explanation for why elevation in CRP and other serum inflammatory markers should be prognostic for coronary artery disease. As discussed by Doggen, C.J.M., *et al.*, one or more of the following factors were speculated to account for the correlation observed: (1) intrinsic inflammation and tissue damage within arterial lesions, (2) prior infection by *Helicobacter pylori* or by *Chlamydia pneumoniae*, (3) release of peptide cytokines including interleukin-6, or (4) activation of the complement system.

15 The end products of the leukotriene pathway are potent inflammatory lipid mediators derived from arachidonic acid. They can potentially contribute to development of atherosclerosis and destabilization of atherosclerotic plaques through lipid oxidation and/or proinflammatory effects. LTC₄, LTD₄, and LTE₄, are known to induce vasoconstriction. Allen *et al.*, *Circulation*, 97:2406-2413 (1998) described a novel mechanism in which atherosclerosis is associated with the appearance of a leukotriene receptor(s) capable of inducing hyperactivity of human epicardial coronary arteries in response to LTC₄ and LTD₄. LTB₄, on the other hand, is a strong proinflammatory agent.

20 Increased production of these end products, of the leukotriene pathway, could therefore serve as a risk factor for MI and atherosclerosis, whereas both inflammation and vasoconstriction/vasospasm have a well established role in the pathogenesis of MI and atherosclerosis. It has also been shown that a heterozygous deficiency of the 5-LO enzyme in a knockout mouse model decreases atherosclerotic lesion size in LDLR^{-/-} mice by about 95%.

25 (Mehrabian *et al.*, *Circulation Research*. 91:120 (2002)). However, such

genetic evidence for leukotriene involvement in MI or atherosclerosis in humans has not been reported. Mehrabian et al. did report a very small genetic association study looking for correlation between promoter polymorphisms of 5-LO and carotid intimal thickening in normal individuals. However, their data paradoxically suggest that a lower amount of leukotriene production correlates with carotid atherosclerosis.

SUMMARY OF THE INVENTION

As described herein, a gene on chromosome 13q12 has been identified as playing a major role in myocardial infarction (MI). This gene, herein after referred to as the MI gene, comprises nucleic acid that encodes 5-lipoxygenase activating protein (ALOX5AP or FLAP,) herein after referred to as FLAP.

The invention pertains to methods of treatment (prophylactic and/or therapeutic) for certain diseases and conditions (*e.g.*, MI, ACS, atherosclerosis) associated with FLAP or with other members of the leukotriene pathway (*e.g.*, biosynthetic enzymes such as FLAP, arachidonate 4-lipoxygenase (5-LO), leukotriene C4 synthetase (LTC4S), leukotriene A4 hydrolase (LTA4H), leukotriene B4 12-hydroxydehydrogenase (LTB4DH)); receptors and/or binding agents of the enzymes; and receptors for the leukotrienes LTA4, LTB4, LTC4, LTD4, LTE4, Cys LT1, Cys LT2, including leukotriene B4 receptor 1 (BLT1), leukotriene B4 receptor 2 (BLT2), cysteinyl leukotriene receptor 1 (CysLTR1), cysteinyl leukotriene receptor 2 (CysLTR2). The methods include the following: methods of treatment for myocardial infarction or susceptibility to myocardial infarction; for acute coronary syndrome (*e.g.*, unstable angina, non-ST-elevation myocardial infarction (NSTEMI) or ST-elevation myocardial infarction (STEMI)); for decreasing risk of a second myocardial infarction; for atherosclerosis, such as for patients requiring treatment (*e.g.*, angioplasty, stents, coronary artery bypass graft) to restore blood flow in arteries (*e.g.*, coronary arteries); and/or for decreasing leukotriene synthesis (*e.g.*, for treatment of myocardial infarction).

In the methods of the invention, a leukotriene synthesis inhibitor is administered to an individual in a therapeutically effective amount. The leukotriene synthesis inhibitor can be an agent that inhibits or antagonizes a member of the leukotriene synthesis pathway (*e.g.*, FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH). For example, the leukotriene synthesis inhibitor can be an agent that inhibits or antagonizes FLAP polypeptide activity (*e.g.*, a FLAP inhibitor) and/or FLAP nucleic acid expression, as described herein (*e.g.*, a FLAP nucleic acid antagonist). In another embodiment, the leukotriene synthesis inhibitor is an agent that inhibits or antagonizes polypeptide activity and/or nucleic acid expression of another member of the leukotriene biosynthetic pathway (*e.g.*, LTC4S, LTA4H, LTB4DH). In preferred embodiments, the agent alters activity and/or nucleic acid expression of FLAP or of 5-LO. Preferred agents include those set forth in the Agent Table herein. In another embodiment, preferred agents can be: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio)-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues; or can be zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues. In another embodiment, the agent alters metabolism or activity of a leukotriene (*e.g.*, LTA4, LTB4, LTC4, LTD4, LTE4, Cys LT1, Cys LT2), such as leukotriene antagonists or antibodies to leukotrienes, as well as agents

which alter activity of a leukotriene receptor (*e.g.*, : BLT1, BLT2, CysLTR1, and CysLTR2).

In certain embodiments of the invention, the individual is an individual who has at least one risk factor, such as an at-risk haplotype for myocardial infarction; an at-risk haplotype in the FLAP gene; a polymorphism in a FLAP nucleic acid; an at-risk polymorphism in the 5-LO gene promoter, diabetes; hypertension; hypercholesterolemia; elevated lp(a); obesity; a past or current smoker; an elevated inflammatory marker (*e.g.*, a marker such as C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9); increased LDL cholesterol and/or decreased HDL cholesterol; increased leukotriene synthesis; and/or at least one previous myocardial infarction, ACS, stable angina, atherosclerosis, requires treatment for restoration of coronary artery blood flow (*e.g.*, angioplasty, stent, coronary artery bypass graft).

The invention pertains to use of leukotriene synthesis inhibitors for the manufacture of a medicament for the treatment of MI, ACS, and/or atherosclerosis, as described herein, as well as for the manufacture of a medicament for the reduction of leukotriene synthesis.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows the multipoint non-parametric LOD scores of a linkage scan of 160 female patients in large extended pedigrees and genotyped using a 1000 framework map on chromosome 13. A LOD score suggestive of linkage of 2.5 was found at marker D13S289. The marker map for chromosome 13 that was used in the linkage analysis is shown in Table 1.

FIG. 2 shows LOD score results for the families after adding 14 additional markers to the candidate region. The inclusion of additional

microsatellite markers increased the information on sharing by decent from 0.7 to 0.8, around the markers that gave the highest LOD scores. The marker map used in the second step of linkage analysis is shown in Table 2.

FIG. 3A shows the results from a haplotype association case-control analysis of 437 female MI patients versus 721 controls using combinations 4 and 5 microsatellite markers to define the test haplotypes. The p -value of the association is plotted on the y-axis and position of markers on the x-axis. Only haplotypes that show association with a p -value $< 10^{-5}$ are shown in the figure. The most significant microsatellite marker haplotype association is found using markers DG13S1103, DG13S166, DG13S1287, DG13S1061 and DG13S301, with alleles 4, 0, 2, 14 and 3, respectively (p -value of 1.02×10^{-7}). Carrier frequency of the haplotype is 7.3% in female MI patients and 0.3% in controls. The segment that is common to all the haplotypes shown in the figure includes only one gene, FLAP.

FIG. 3B shows the alleles of the markers defining the most significant microsatellite marker haplotypes. The segment defined with a black square is common to all the of most significantly associated haplotypes. The FLAP nucleic acid is located between makers DG13S166 and D13S1238. Two marker haplotype involving alleles 0 and -2 for markers DG13S166 and D13S1238, respectively, is found in excess in patients. Carrier frequency of this haploype is 27% in patients and 15.4% in controls (p -value 1×10^{-3}). Therefore, association analysis confirms that the most tightly MI-associated gene within the linkage peak is FLAP.

FIG. 4 shows the markers and genes around the FLAP (ALOX5AP) gene.

FIG. 5 shows the relative location of key SNPs and exons of the ALOX5AP/FLAP gene (exons shown in vertical rectangles). Haplotype length varies between 33 to 68 kb.

FIG. 6A-6Y4 show the genomic sequence of the FLAP gene (SEQ ID NO: 1).

-12-

FIG. 7 shows the amino acid sequence of FLAP (SEQ ID NO:2) and the mRNA of FLAP (SEQ ID NO: 3).

FIG. 8A-8U show the sequences of the FLAP nucleic acid flanking the SNPs that were identified by sequencing samples from patients (SEQ ID NOs: 398-535).

FIG. 9 shows a significant positive correlation between serum LTE4 levels and serum CRP levels.

DETAILED DESCRIPTION OF THE INVENTION

Extensive genealogical information has been combined with powerful gene sharing methods to map a gene on chromosome 13q12 that is associated with myocardial infarction. A genome wide search for susceptibility genes for MI, using a framework map of 1000 microsatellite markers, revealed a locus suggestive of linkage on 13q12. Sixty families with 159 female MI patients that clustered within and including 6 meiotic events were used in linkage analysis. At first, only female MI patients were used in the linkage analysis in an effort to enrich for patients with stronger genetic factors contributing to their risk for MI. The epidemiological study of a population-based sample of Icelandic MI patients had previously suggested that the genetic factors for MI might be stronger for females than males, as the relative risk for siblings of female MI patients was significantly higher than the relative risk for siblings of male probands (1.59 (CI 1.47 - 1.73) vs. 1.35 (CI 1.28 - 1.42)) (unpublished data). The highest LOD score (2.5) was found at marker D13S289. The LOD score results for the families remained the same after adding 14 microsatellite markers to the candidate region. The inclusion of the additional markers increased the information on sharing by descent from 0.7 to 0.8, around the markers that gave the highest LOD scores. This linkage analysis mapped a gene contributing to MI to chromosome 13q12.

The candidate MI locus on chromosome 13q12 was then finely mapped with microsatellite markers. Patients with myocardial infarction and

controls were initially genotyped with microsatellite markers with an average spacing between markers of less than 100Kb over the 12Mb candidate region. Initial haplotype association analysis that included all genotyped microsatellite markers across the MI candidate locus, resulted in several extended haplotypes composed of 4 and 5 microsatellite markers that were significantly associated with female MI (see, *e.g.*, Tables 4 and 5 below). A region common to all these extended haplotypes, is defined by markers DG13S166 and D13S1238. This region includes only one gene, the FLAP nucleic acid sequence. The two marker haplotype involving alleles 0 and -2 for markers DG13S166 and D13S1238, respectively, was found in excess in patients. Specific variants of the gene were then sought that were associated with MI.

In order to screen for SNPs in the FLAP gene, the whole gene was sequenced, both exons and introns. Initially, 9 SNPs identified within the gene were genotyped in patients and controls. Additional microsatellite markers close to or within the FLAP gene were also genotyped in all patients and controls. Five publicly known SNPs that are located within a 200Kb distance 5' to the FLAP gene were also genotyped in patients and controls. Haplotype association analysis in this case-control study including these additional markers showed several different variants of the same haplotype that were all significantly associated with female MI (see, *e.g.*, Table 6). Table 7 shows two haplotypes that are representative of these female MI risk haplotypes which are referred to herein as the female MI "at risk" haplotypes. The relative risk for male MI patients that had the female MI-"at risk" haplotype was increased (see, *e.g.*, Table 7), indicating that the female MI-"at risk" haplotype also increased the risk of having an MI in males. These results further strengthened the hypothesis that the FLAP gene was an MI susceptibility gene.

SNP haplotype association to MI

In an effort to identify haplotypes involving only SNP markers that associate with MI, additional SNPs were identified by sequencing the FLAP

gene and the region flanking the gene. Currently, a total of 45 SNPs in 1343 patients and 624 unrelated controls have been genotyped. Two correlated series of SNP haplotypes have been observed in excess in patients, denoted as A and B in Table 9. The length of the haplotypes varies between 33 and 69 Kb, and the haplotypes cover one or two blocks of linkage disequilibrium. Both series of haplotypes contain the common allele 2 of the SNP SG13S25. All haplotypes in the A series contain the SNP DG00AAHID, while all haplotypes in the B series contain the SNP DG00AAHII. In the B series, the haplotypes B4, B5, and B6 have a relative risk (RR) greater than 2 and with allelic frequencies above 10%. The haplotypes in the A series have slightly lower RR and lower p-values, but higher frequency (15-16%). The haplotypes in series B and A are strongly correlated, i.e. the haplotypes in B define a subset of the haplotypes in A. Hence, haplotypes in series B are more specific than A. However, haplotypes in series A are more sensitive, i.e. they capture more individuals with the putative mutation, as is observed in the population attributable risk which is less for B than for A. Furthermore, these haplotypes show similar risk ratios and allelic frequencies for early-onset patients (defined as onset of first MI before the age of 55) and for both genders. In addition, analyzing various groups of patients with known risk factors, such as hypertension, high cholesterol, smoking and diabetes, do not reveal any significant correlation with these haplotypes, suggesting that the haplotypes in the FLAP gene represent an independent genetic susceptibility factor for MI.

The FLAP nucleic acid encodes a 5-lipoxygenase activating protein, which, in combination with 5-lipoxygenase (5-LO), is required for leukotriene synthesis. FLAP acts coordinately with 5-LO to catalyze the first step in the synthesis of leukotrienes from arachidonic acid. It catalyzes the conversion of arachidonic acid to 5(S)-hydroperoxy-6-trans-8,11,14-cis-eicosatetraenoic acid (5-HPETE), and further to the allylic epoxide 5 (S)-trans7,9 trans 11,14-cis-eicosatetraenoic acid (leukotriene A4, LTA4).

The leukotrienes are a family of highly potent biological mediators of inflammatory processes produced primarily by bone marrow derived

leukocytes such as monocytes, macrophages, and neutrophils. Both FLAP and 5-LO are detected within atherosclerosis lesions, indicating that the vessel itself can be a source of leukotrienes. It is demonstrated herein that the MI-risk FLAP haplotype is associated with higher serum leukotriene levels.

5 Increased production of leukotriene in individuals with pre-existing atherosclerosis lesions may lead to plaque instability or friability of the fibrous cap leading to local thrombotic events. If this occurs in coronary artery arteries it leads to MI or unstable angina. If it occurs in the cerebrovasculature it leads to stroke or transient ischemic attack. If it occurs in large arteries to
10 the limbs, it causes or exacerbates limb ischemia in persons with peripheral arterial occlusive disease. Therefore, those with genetically influenced predisposition to produce higher leukotriene levels have higher risk for events due to pre-existing atherosclerosis such as MI.

Inhibitors of FLAP function impede translocation of 5-LO from the cytoplasm to the cell membrane and inhibit activation of 5-LO and thereby
15 decrease leukotriene synthesis.

As a result of these discoveries, methods are now available for the treatment of myocardial infarction (MI) and acute coronary syndrome (ACS) through the use of leukotriene inhibitors, such as agents that inhibit
20 leukotriene biosynthesis or antagonize signaling through leukotriene receptors. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease or condition, but also preventing or delaying the onset of the disease or condition; preventing or delaying the occurrence of a second episode of the disease or condition; and/or also
25 lessening the severity or frequency of symptoms of the disease or condition. In the case of atherosclerosis, "treatment" also refers to a minimization or reversal of the development of plaques. Methods are additionally available for assessing an individual's risk for MI or ACS. In preferred embodiment, the individual to be treated is an individual who is susceptible (at increased risk)
30 for MI or ACS, such as an individual who is in one of the representative target populations described herein.

REPRESENTATIVE TARGET POPULATIONS

In one embodiment of the invention, an individual who is at risk for MI or ACS is an individual who has an at-risk haplotype in FLAP, as described herein. In one embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers DG00AAFIU, SG13S25, DG00AAJFF, DG00AAHII, SG13S32 and SG13S35 at the 13q12 locus. In another embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers DG00AAFIU, SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In a third embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In a fourth embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers DG00AAFIU, SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus. In a fifth embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus. Increased risk for MI or ACS in individuals with a FLAP at-risk haplotype is logically conferred by increased production of leukotrienes in the arterial vessel wall or in bone-marrow derived inflammatory cells within the blood and/or arterial vessel wall. It is shown herein that FLAP at-risk haplotypes are associated with high serum leukotriene E4 levels. It is further shown herein that serum leukotriene levels (specifically, leukotrieneE4) correlate with serum CRP levels in myocardial infarction patients. Therefore, FLAP genetic variation drives high leukotriene levels (within the blood vessel and/or systemically) which in turn drive higher CRP levels which has been shown as a risk factor for MI. Accordingly, individuals with a FLAP at-risk haplotype are likely to have elevated serum C-reactive protein. The level of serum C-reactive protein can be used as a surrogate for the level of arterial wall inflammation initiated

by lipid deposition and atherogenesis conferred by the presence of the at-risk FLAP haplotype.

In another embodiment of the invention, an individual who is at risk for MI or ACS is an individual who has a polymorphism in a FLAP gene, in which the presence of the polymorphism is indicative of a susceptibility to MI or ACS. The term "gene," as used herein, refers to not only the sequence of nucleic acids encoding a polypeptide, but also the promoter regions, transcription enhancement elements, splice donor/acceptor sites, and other non-transcribed nucleic acid elements. Representative polymorphisms include those presented in Table 3, below.

In a further embodiment of the invention, an individual who is at risk for MI or ACS is an individual who has an at-risk polymorphism in the 5-LO gene in the promoter region, as described herein.

In a fourth embodiment, an individual who is at risk for MI or ACS is an individual who has an elevated inflammatory marker. An "elevated inflammatory marker," as used herein, is the presence of an amount of an inflammatory marker that is greater, by an amount that is statistically significant, than the amount that is typically found in control individual(s) or by comparison of disease risk in a population associated with the lowest band of measurement (*e.g.*, below the mean or median, the lowest quartile or the lowest quintile) compared to higher bands of measurement (*e.g.*, above the mean or median, the second, third or fourth quartile; the second, third, fourth or fifth quintile). An "inflammatory marker" refers to a molecule that is indicative of the presence of inflammation in an individual, for example, C-reactive protein (CRP), serum amyloid A, fibrinogen, leukotriene levels (*e.g.*, leukotriene E4), leukotriene metabolites (*e.g.*, cysteinyl leukotriene 1), interleukin-6, tissue necrosis factor-alpha, soluble vascular cell adhesion molecules (sVCAM), soluble intervascular adhesion molecules (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9) or other markers (see, *e.g.*, Doggen, C.J.M. *et al.*, *J. Internal Med.*, 248:406-414 (2000);

Ridker, P.M. *et al.*, *New Englnd. J. Med.* 1997: 336: 973-979, Rettersol, L. *et al.*, 2002: 160:433-440; Ridker, P.M. *et al.*, *New England. J. Med.*, 2002: 347: 1557-1565; Bermudez, E.A. *et al.*, *Arterioscler. Thromb. Vasc. Biol.*, 2002: 22:1668-1673). In certain embodiments, the presence of such inflammatory markers can be measured in serum or urine.

In a fifth embodiment, an individual who is at risk for MI or ACS is an individual who has increased LDL cholesterol and/or decreased HDL cholesterol levels. For example, the American Heart Association indicates that an LDL cholesterol level of less than 100 mg/dL is optimal; from 100-129 mg/dL is near/above optimal; from 130-159 mg/dL is borderline high; from 160-189 is high; and from 190 and up is very high. Therefore, an individual who is at risk for MI or ACS because of an increased LDL cholesterol level is, for example, an individual who has more than 100 mg/dL cholesterol, such as an individual who has a near/above optimal level, a borderline high level, a high level or a very high level. Similarly, the American Heart Association indicates that an HDL cholesterol level of less than 40 mg/dL is a major risk factor for heart disease; and an HDL cholesterol level of 60 mg/dL or more is protective against heart disease. Thus, an individual who is at risk for MI or ACS because of a decreased HDL cholesterol level is, for example, an individual who has less than 60 mg/dL HDL cholesterol, such as an individual who has less than 40 mg/dL HDL cholesterol.

In a sixth embodiment, an individual who is at risk for MI or ACS is an individual who has increased leukotriene synthesis. "Increased leukotriene synthesis," as used herein, indicates an amount of production of leukotrienes that is greater, by an amount that is statistically significant, than the amount of production of leukotrienes that is typically found in control individual(s) or by comparison of leukotriene production in a population associated with the lowest band of measurement (*e.g.*, below the mean or median, the lowest quartile or the lowest quintile) compared to higher bands of measurement (*e.g.*, above the mean or median, the second, third or fourth quartile; the second, third, fourth or fifth quintile). For example, the FLAP at-risk

haplotypes correlate with increased serum leukotriene synthesis levels. An individual can be assessed for the presence of increased leukotriene synthesis by a variety of methods. For example, an individual can be assessed for an increased risk of MI, ACS or atherosclerosis, by assessing the level of a leukotriene metabolite (e.g., LTE4) in a sample (e.g., serum, plasma or urine) from the individual. An increased level of leukotriene metabolites is indicative of increased production of leukotrienes, and of an increased risk of MI, ACS or atherosclerosis.

In a further embodiment, an individual who is at risk for MI or ACS is an individual who has already experienced at least one MI or ACS event, or who has stable angina, and is therefore at risk for a second MI or ACS event. In another embodiment, an individual who is at risk for MI or ACS is an individual who has atherosclerosis or who requires treatment (e.g., angioplasty, stents, coronary artery bypass graft) to restore blood flow in arteries.

In additional embodiments, an individual who is at risk for MI or ACS is an individual who has diabetes; hypertension; hypercholesterolemia; elevated lip(a); obesity; and/or is a past or current smoker.

Individuals at risk for MI or ACS may fall into more than one of these representative target populations. For example, an individual may have experienced at least one MI or ACS event, and may also have an increased level of an inflammatory marker. As used therein, the term "individual in a target population" refers to an individual who is at risk for MI or ACS who falls into at least one of the representative target populations described above.

ASSESSMENT FOR AT-RISK HAPLOTYPES

A "haplotype," as described herein, refers to a combination of genetic markers ("alleles"), such as those set forth in Table 3. In a certain embodiment, the haplotype can comprise one or more alleles, two or more alleles, three or more alleles, four or more alleles, or five or more alleles. The genetic markers are particular "alleles" at "polymorphic sites" associated with

FLAP. A nucleotide position at which more than one sequence is possible in a population (either a natural population or a synthetic population, *e.g.*, a library of synthetic molecules), is referred to herein as a "polymorphic site". Where a polymorphic site is a single nucleotide in length, the site is referred to as a single nucleotide polymorphism ("SNP"). For example, if at a particular chromosomal location, one member of a population has an adenine and another member of the population has a thymine at the same position, then this position is a polymorphic site, and, more specifically, the polymorphic site is a SNP. Polymorphic sites can allow for differences in sequences based on substitutions, insertions or deletions. Each version of the sequence with respect to the polymorphic site is referred to herein as an "allele" of the polymorphic site. Thus, in the previous example, the SNP allows for both an adenine allele and a thymine allele.

Typically, a reference sequence is referred to for a particular sequence. Alleles that differ from the reference are referred to as "variant" alleles. For example, the reference FLAP sequence is described herein by SEQ ID NO:1. The term, "variant FLAP", as used herein, refers to a sequence that differs from SEQ ID NO:1, but is otherwise substantially similar. The genetic markers that make up the haplotypes described herein are FLAP variants.

Additional variants can include changes that affect a polypeptide, *e.g.*, the FLAP polypeptide. These sequence differences, when compared to a reference nucleotide sequence, can include the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of a reading frame; duplication of all or a part of a sequence; transposition; or a rearrangement of a nucleotide sequence, as described in detail above. Such

sequence changes alter the polypeptide encoded by a FLAP nucleic acid. For example, if the change in the nucleic acid sequence causes a frame shift, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with MI or a susceptibility to MI can be a synonymous change in one or more nucleotides (*i.e.*, a change that does not result in a change in the amino acid sequence). Such a polymorphism can, for example, alter splice sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the polypeptide. The polypeptide encoded by the reference nucleotide sequence is the "reference" polypeptide with a particular reference amino acid sequence, and polypeptides encoded by variant alleles are referred to as "variant" polypeptides with variant amino acid sequences.

Haplotypes are a combination of genetic markers, *e.g.*, particular alleles at polymorphic sites. The haplotypes described herein, *e.g.*, having markers such as those shown in Table 3, are found more frequently in individuals with MI than in individuals without MI. Therefore, these haplotypes have predictive value for detecting MI or a susceptibility to MI in an individual. The haplotypes described herein are in some cases a combination of various genetic markers, *e.g.*, SNPs and microsatellites. Therefore, detecting haplotypes can be accomplished by methods known in the art for detecting sequences at polymorphic sites, such as the methods described above.

In certain methods described herein, an individual who is at risk for MI or ACS is an individual in whom an at-risk haplotype is identified. In one embodiment, the at-risk haplotype is one that confers a significant risk of MI. In one embodiment, significance associated with a haplotype is measured by an odds ratio. In a further embodiment, the significance is measured by a percentage. In one embodiment, a significant risk is measured as an odds ratio of at least about 1.2, including by not limited to: 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, and 1.9. In a further embodiment, an odds ratio of at least 1.2 is significant.

In a further embodiment, an odds ratio of at least about 1.5 is significant. In a further embodiment, a significant increase in risk is at least about 1.7 is significant. In a further embodiment, a significant increase in risk is at least about 20%, including but not limited to about 25%, 30%, 35%, 40%, 45%,
5 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, and 98%. In a further embodiment, a significant increase in risk is at least about 50%. It is understood however, that identifying whether a risk is medically significant may also depend on a variety of factors, including the specific disease, the haplotype, and often, environmental factors.

10 An at-risk haplotype in, or comprising portions of, the FLAP gene, in one where the haplotype is more frequently present in an individual at risk for MI or ACS (affected), compared to the frequency of its presence in a healthy individual (control), and wherein the presence of the haplotype is indicative of MI or ACS or susceptibility to MI or ACS. Standard techniques for
15 genotyping for the presence of SNPs and/or microsatellite markers can be used, such as fluorescent based techniques (Chen, *et al.*, *Genome Res.* 9, 492 (1999)), PCR, LCR, Nested PCR and other techniques for nucleic acid amplification. In a preferred embodiment, the method comprises assessing in
20 an individual the presence or frequency of SNPs and/or microsatellites in, comprising portions of, the FLAP gene, wherein an excess or higher frequency of the SNPs and/or microsatellites compared to a healthy control individual is indicative that the individual has MI or ACS, or is susceptible to MI or ACS. See, for example, Table 3 (below) for SNPs and markers that can form
25 haplotypes that can be used as screening tools. These markers and SNPs can be identified in at-risk haplotypes. For example, an at-risk haplotype can include microsatellite markers and/or SNPs such as those set forth in Table 3. The presence of the haplotype is indicative of MI or ACS, or a susceptibility to MI or ACS, and therefore is indicative of an individual who falls within a target population for the treatment methods described herein.

30 Haplotype analysis involves defining a candidate susceptibility locus using LOD scores. The defined regions are then ultra-fine mapped with

microsatellite markers with an average spacing between markers of less than 100Kb. All usable microsatellite markers that found in public databases and mapped within that region can be used. In addition, microsatellite markers identified within the deCODE genetics sequence assembly of the human genome can be used. The frequencies of haplotypes in the patient and the control groups using an expectation-maximization algorithm can be estimated (Dempster A. *et al.*, 1977. *J. R. Stat. Soc. B*, 39:1-389). An implementation of this algorithm that can handle missing genotypes and uncertainty with the phase can be used. Under the null hypothesis, the patients and the controls are assumed to have identical frequencies. Using a likelihood approach, an alternative hypothesis where a candidate at-risk-haplotype, which can include the markers described herein, is allowed to have a higher frequency in patients than controls, while the ratios of the frequencies of other haplotypes are assumed to be the same in both groups is tested. Likelihoods are maximized separately under both hypotheses and a corresponding 1-df likelihood ratio statistics is used to evaluate the statistic significance.

To look for at-risk-haplotypes in the 1-lod drop, for example, association of all possible combinations of genotyped markers is studied, provided those markers span a practical region. The combined patient and control groups can be randomly divided into two sets, equal in size to the original group of patients and controls. The haplotype analysis is then repeated and the most significant p-value registered is determined. This randomization scheme can be repeated, for example, over 100 times to construct an empirical distribution of p-values.

In one embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers DG00AAFTU, SG13S25, DG00AAJFF, DG00AAHII, SG13S32 and SG13S35 at the 13q12 locus. In another embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers DG00AAFTU, SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In a third embodiment, a haplotype associated with a susceptibility to myocardial

infarction comprises markers SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In a fourth embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers DG00AAFIU, SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus.

METHODS OF THERAPY

The present invention encompasses methods of treatment (prophylactic and/or therapeutic) for MI or ACS in individuals, such as individuals in the target populations described above, as well as for other diseases and conditions associated with FLAP or with other members of the leukotriene pathway (*e.g.*, for atherosclerosis). Members of the "leukotriene pathway," as used herein, include polypeptides (*e.g.*, enzymes, receptors) and other molecules that are associated with production of leukotrienes: for example, enzymes such as FLAP, 5-LO, other leukotriene biosynthetic enzymes (*e.g.*, leukotriene C4 synthetase, leukotriene A4 hydrolase); receptors or binding agents of the enzymes; leukotrienes such as LTA4, LTB4, LTC4, LTD4, LTE4, Cys LT1, and Cys LT2; and receptors of leukotrienes (*e.g.*, leukotriene B4 receptor 1 (BLT1), leukotriene B4 receptor 2 (BLT2), cysteinyl leukotriene receptor 1 (CysLTR1), cysteinyl leukotriene receptor 2 (CysLTR2)).

In particular, the invention relates to methods of treatment for myocardial infarction or susceptibility to myocardial infarction (for example, for individuals in an at-risk population such as those described above); as well as methods of treatment for acute coronary syndrome (*e.g.*, unstable angina, non-ST-elevation myocardial infarction (NSTEMI) or ST-elevation myocardial infarction (STEMI)); for decreasing risk of a second myocardial infarction; for atherosclerosis, such as for patients requiring treatment (*e.g.*, angioplasty, stents, coronary artery bypass graft) to restore blood flow in arteries (*e.g.*, coronary arteries); and/or for decreasing leukotriene synthesis (*e.g.*, for treatment of MI or ACS).

The invention additionally pertains to use of one or more leukotriene synthesis inhibitors, as described herein, for the manufacture of a medicament for the treatment of MI, ACS, and/or atherosclerosis, e.g., using the methods described herein.

5 In the methods of the invention, a "leukotriene synthesis inhibitor" is used.

In one embodiment, a "leukotriene synthesis inhibitor" is an agent that inhibits FLAP polypeptide activity and/or FLAP nucleic acid expression, as described herein (e.g., a nucleic acid antagonist). In another embodiment, a
10 leukotriene synthesis inhibitor is an agent that inhibits polypeptide activity and/or nucleic acid expression of another member of the leukotriene biosynthetic pathway (e.g., 5-LO; LTC4S; LTA4H; LTB4DH). In still another embodiment, a leukotriene synthesis inhibitor is an agent that alters activity or metabolism of a leukotriene (e.g., an antagonist of a leukotriene; an
15 antagonist of a leukotriene receptor). In preferred embodiments, the leukotriene synthesis inhibitor alters activity and/or nucleic acid expression of FLAP or of 5-LO, or alters interaction between FLAP and 5-LO.

Leukotriene synthesis inhibitors can alter polypeptide activity or nucleic acid expression of a member of the leukotriene pathway by a variety
20 of means, such as, for example, by catalytically degrading, downregulating or interfering with the expression, transcription or translation of a nucleic acid encoding the member of the leukotriene pathway; by altering posttranslational processing of the polypeptide; by altering transcription of splicing variants; or by interfering with polypeptide activity (e.g., by binding to the polypeptide, or
25 by binding to another polypeptide that interacts with that member of the leukotriene pathway, such as a FLAP binding agent as described herein or some other binding agent of a member of the leukotriene pathway; by altering interaction among two or more members of the leukotriene pathway (e.g., interaction between FLAP and 5-LO); or by antagonizing activity of a member
30 of the leukotriene pathway.

Representative leukotriene synthesis inhibitors include the following:

agents that inhibit activity of a member of the leukotriene biosynthetic pathway (*e.g.*, FLAP, 5-LO), LTC4S, LTA4H, LTB4DH, such as the agents presented in the Agent Table below;

agents that inhibit activity of receptors of members of the leukotriene pathway, such as FLAP receptors, LTA4 receptors, LTB4 receptors, LTC4 receptors, LTD4 receptors, TLE4 receptors, Cys LT1 receptors, Cys LT2 receptors, 5-LO receptors; BLT1; BLT2; CysLTR1; CysLTR2; agents that bind to the members of the leukotriene pathway, such as FLAP binding agents (*e.g.*, 5-LO), agents that bind to receptors of members of the leukotriene pathway (*e.g.*, leukotriene receptor antagonists); or agents that bind to a leukotriene (*e.g.*, to LTA4, LTB4, LTC4, LTD4, LTE4, Cys LT1, Cys LT2) or otherwise affect (*e.g.*, increase or decrease) activity of the leukotriene;

antibodies to leukotrienes;

antisense nucleic acids or small double-stranded interfering RNA, to nucleic acids encoding FLAP, 5-LO, or a leukotriene synthetase or other member of the leukotriene pathway, or fragments or derivatives thereof, including antisense nucleic acids to nucleic acids encoding the FLAP, 5-LO or leukotriene synthetase polypeptides, and vectors comprising such antisense nucleic acids (*e.g.*, nucleic acid, cDNA, and/or mRNA, double-stranded interfering RNA, or a nucleic acid encoding an active fragment or derivative thereof, or an oligonucleotide; for example, the complement of one of SEQ ID Nos. 1 or 3, or a nucleic acid complementary to the nucleic acid encoding SEQ ID NO: 2, or fragments or derivatives thereof);

peptidomimetics; fusion proteins or prodrugs thereof; ribozymes; other small molecules; and

5 other agents that alter (*e.g.*, inhibit or antagonize) expression of a member of the leukotriene pathway, such as FLAP or 5-LO nucleic acid expression or polypeptide activity, or that regulate transcription of FLAP splicing variants or 5-LO splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed).

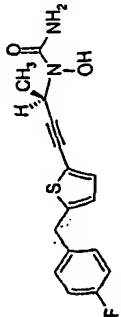
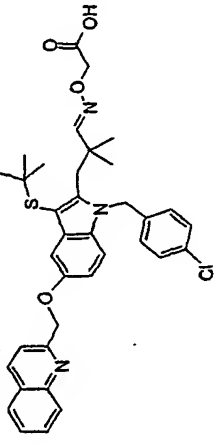
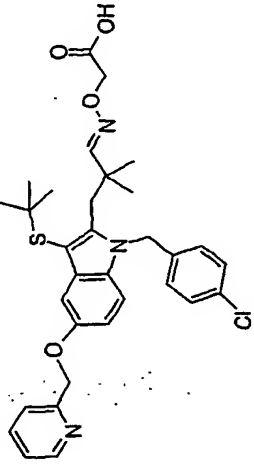
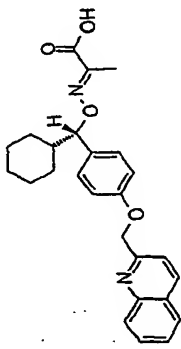
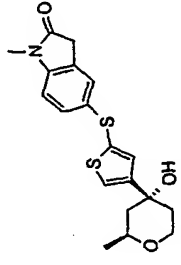
10 More than one leukotriene synthesis inhibitor can be used concurrently, if desired.

The therapy is designed to alter activity of a FLAP polypeptide, a 5-LO polypeptide, or another member of the leukotriene pathway in an individual, such as by inhibiting or antagonizing activity. For example, a
15 leukotriene synthesis inhibitor can be administered in order to decrease synthesis of leukotrienes within the individual, or to downregulate or decrease the expression or availability of the FLAP nucleic acid or specific splicing variants of the FLAP nucleic acid. Downregulation or decreasing expression or availability of a native FLAP nucleic acid or of a particular splicing variant
20 could minimize the expression or activity of a defective nucleic acid or the particular splicing variant and thereby minimize the impact of the defective nucleic acid or the particular splicing variant. Similarly, for example, a leukotriene synthesis inhibitor can be administered in order to downregulate or decrease the expression or availability of the nucleic acid encoding 5-LO or
25 specific splicing variants of the nucleic acid encoding 5-LO.

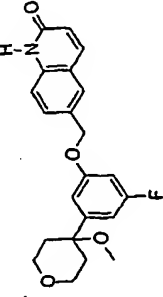
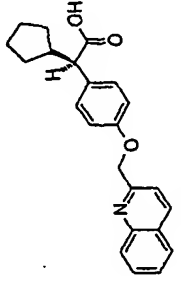
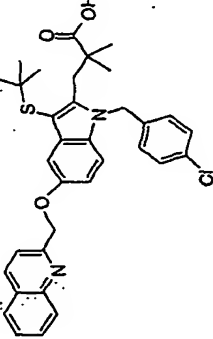
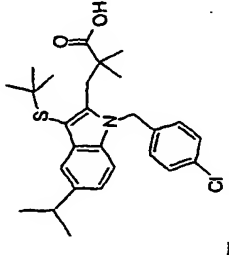
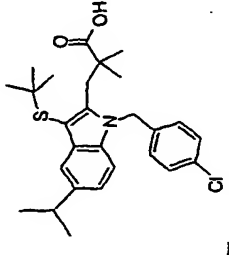
The leukotriene synthesis inhibitor(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease or condition, such as by ameliorating symptoms associated with the
30 disease or condition, preventing or delaying the onset of the disease or condition, and/or also lessening the severity or frequency of symptoms of the

disease or condition). The amount which will be therapeutically effective in the treatment of a particular individual's disease or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In preferred embodiments of the invention, the leukotriene synthesis inhibitor agent is an agent that inhibits activity of FLAP and/or of 5-LO. Preferred agents include the following, as set forth in the Agent Table:

Company	Product Name (Code)	Structure	Chemical Name	Patent Ref	Date Patent Issued/Applica tion Published	MOA
Abbott	alreleuton (ABT-761)		(R)-(+)-N-[3-((4-fluorophenyl)methyl)-2-phenyl]-1-methyl-2-propenyl]-N-hydroxyurea	US 5288751, US 5288743, US 5616596	2/22/94 04/01/97	5-LPO Inhibitor
Abbott	A-81834		3-((3-(1,1-dimethylethylthio)-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid	WO9203132, US 5459150	3/5/1992, 10/17/95	FLAP Inhibitor
Abbott	A-86886		3-((3-(1,1-dimethylethylthio)-5-(pyridin-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid	WO9203132, US 5459150	3/5/1992, 10/17/95	5-LPO Inhibitor
Abbott	A-93178					FLAP Inhibitor
AstraZeneca	AZD-4407			EP 623614	09/11/94	5-LPO Inhibitor

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AsiraZeneca	ZD-2138		6-(3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4-yl)phenoxy)methyl-1-methyl-2(1H)-quinolinone (alternatively NH can be N-methyl)	EP 466452		5-LPO inhibitor
Bayer	BAY-X-1005		(R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-benzeneacetic acid	US 5970215 EP 344519, DE 19880531		FLAP inhibitor
Merck	MK-0591		1-(4-chlorophenyl)methyl-3-(1,1-dimethylethylthio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-indole-2-propanoic acid	EP 419049, US 19890822		FLAP inhibitor
Merck	MK-866		(3-(4-chlorophenyl)-3-(1,1-dimethylethylthio)-5-isopropylindol-2-yl)-2,2-dimethylpropanoic acid			5-LPO inhibitor
Merck	MK-866		1-(4-chlorophenyl)methyl-3-(1,1-dimethylethylthio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-indole-2-propanoic acid	EP 419049, US 19890822		5-LPO inhibitor
Pfizer	CJ-13610		4-(3-(4-(2-Methylimidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide			5-LPO inhibitor

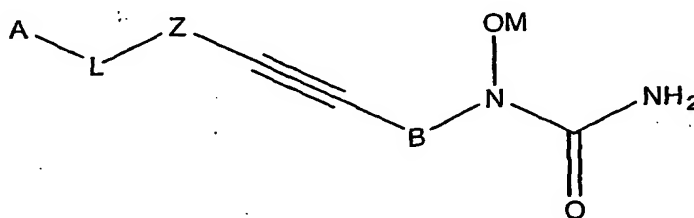
In preferred methods of the invention, the agents set forth in the Agent Table can be used for prophylactic and/or therapeutic treatment for diseases and conditions associated with FLAP or with other members of the leukotriene pathway, or with increased leukotriene synthesis. In particular, they can be used for treatment for myocardial infarction or susceptibility to myocardial infarction, such as for individuals in an at-risk population as described above, (e.g., based on identified risk factors such as elevated cholesterol, elevated C-reactive protein, and/or genotype); for individuals suffering from acute coronary syndrome, such as unstable angina, non-ST-elevation myocardial infarction (NSTEMI) or ST-elevation myocardial infarction (STEMI); for decreasing risk of a subsequent myocardial infarction, such as in individuals who have already had one or more myocardial infarctions; for treatment of atherosclerosis, such as in patients requiring treatment (e.g., angioplasty, stents, coronary artery bypass graft) to restore blood flow in arteries (e.g., coronary arteries); and/or for decreasing leukotriene synthesis (e.g., for treatment of myocardial infarction).

In one preferred embodiment of the invention, the leukotriene synthesis inhibitor is an inhibitor of FLAP such as 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, their optically pure enantiomers, salts, chemical derivatives, analogues, or other compounds inhibiting FLAP that effectively decrease leukotriene biosynthesis when administered to humans.

In another preferred embodiment of the invention, the leukotriene synthesis inhibitor is an inhibitor of 5LO such as zileuton, atreleuton, 6-((3-

fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-
 2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-
 chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha, alpha-dimethyl-5-(2-
 quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886,
 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-
 5 carboxylic acid amide otherwise known as CJ-13610, their optically pure
 enantiomers, salts, chemical derivatives, analogues or other compounds
 inhibiting 5-LO that effectively decrease leukotriene biosynthesis when
 administered to humans.

The compound can be represented by the following formula:

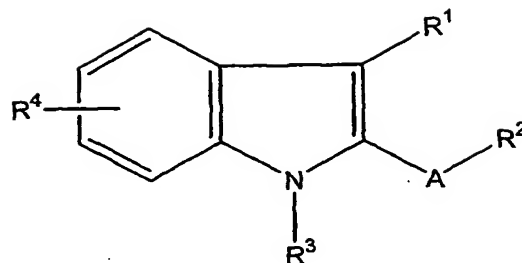


or a pharmaceutically acceptable salt thereof, wherein M is selected from the
 group consisting of hydrogen, a pharmaceutically acceptable cation, and a
 pharmaceutically acceptable metabolically cleavable group; B is a straight or
 branched divalent alkylene group of from one to twelve carbon atoms; Z is
 20 thiazolyl, optionally substituted with alkyl of from one to six carbon atoms or
 haloalkyl of from one to six carbon atoms; L is selected from the group consisting
 of (a) alkylene of from 1-6 carbon atoms, (b) alkenylene of from 2-6 carbon
 atoms, (c) alkynylene of from 2-6 carbon atoms, (d) hydroxyalkyl of 1-6 carbon
 atoms, (e) $>C=O$, (f) $>C=N-OR_1$, where R_1 is hydrogen or C_1-C_6 alkyl, (g) -
 25 $(CHR_1)_n(CO)(CHR_2)_m$, where n and m are independently selected from an integer
 from one to six and R_1 and R_2 are independently selected from hydrogen and C_1-

C₆-alkyl, (h) -(CHR₁)_n C=NOR₂, where R₁, R₂ and n are as defined above; (i) -(CHR₁)_n ON=CR₂, where R₁, R₂ and n are as defined above; (j) -(CHR₁)_n -O-(CHR₂)_m -, where R₁, R₂, n and m are as defined above, (k) -(CHR₁)_n -NR₂(CHR₃)_m -, where R₁, R₂, n and m are as defined above and R₃ is selected from hydrogen and C₁-C₆-alkyl; (l) -(CHR₁)_n -S- (CHR₂)_m -, where R₁, R₂, n and m are as defined above; and (m) -(CHR₁)_n -(SO₂)-(CHR₂)_m -, where R₁, R₂, n and m are as defined above; A is carbocyclic aryl optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, hydroxyalkyl of from one to six carbon atoms, alkoxy of from one to twelve carbon atoms, alkoxyalkoxyl in which the two alkoxy portions may each independently contain from one to six carbon atoms, alkylthio of from one to six carbon atoms, hydroxy, halogen, cyano, amino, alkylamino of from one to six carbon atoms, dialkylamino in which the two alkyl groups may independently contain from one to six carbon atoms, alkanoylamino of from two to eight carbon atoms, N-alkanoyl-N-alkylamino in which the alkanoyl is of from two to eight carbon atoms and the alkyl group is of from one to six carbon atoms, alkylaminocarbonyl of from two to eight carbon atoms, dialkylaminocarbonyl in which the two alkyl groups are independently of from one to six carbon atoms, carboxyl, alkoxycarbonyl or from two to eight carbon atoms, phenyl, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen, phenoxy, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen, and phenylthio, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen. Preferably, the compound is a compound or pharmaceutically acceptable salt thereof having the name (R)-N-{3-[-5-(4-fluorophenylmethyl)thiazo-2-yl]-1methyl-2-propynyl}-N-hydroxyurea. See U.S. Patent No. 4,615,596, incorporated herein by reference.

The compound is represented by the following formula:

-34-

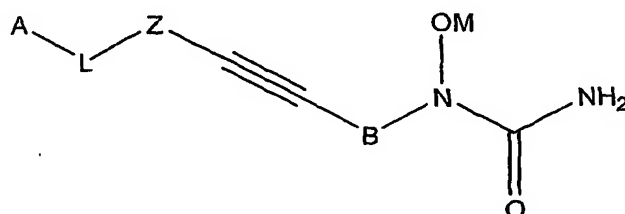


or a pharmaceutically acceptable salt thereof, wherein A is selected from the group consisting of straight or branched divalent alkylene of from one to twelve carbon atoms and divalent cycloalkylene of from three to eight carbon atoms; R₁ is selected from the group consisting of hydrogen, alkylthio of from one to six carbon atoms, phenylthio, optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen, phenylalkylthio in which the alkyl portion contains from one to six carbon atoms, and the phenyl group is optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen, R₂ is selected from the group consisting of -COOB wherein B is selected from hydrogen, a pharmaceutically acceptable cation, or a metabolically cleavable group, -COOalkyl where the alkyl portion contains from one to six carbon atoms, -COOalkylcarbocyclicaryl where the alkyl portion contains from one to six carbon atoms and the aryl portion is optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen, -CONR₅R₆ wherein R₅ is selected from the group consisting of hydrogen, hydroxyl, alkyl of from one to six carbon atoms, and alkoxy of from one to six carbon atoms, and R₆ is selected from the group consisting of hydrogen and alkyl of from one to six carbon atoms, -COR₆, and -OH; R₃ is selected from the group consisting of phenylalkyl in which the alkyl portion contains from one to six carbon atoms, and the phenyl group is optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen, R₄ is selected from the group consisting of thiazolylalkyloxy in which the alkyl portion contains from one to six carbon atoms, and the heteroaryl portion is optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or

halogen, and thiazolyloxy optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen. See U.S. Patent No. 5,288,743, incorporated herein by reference.

The compound can be represented by the formula:

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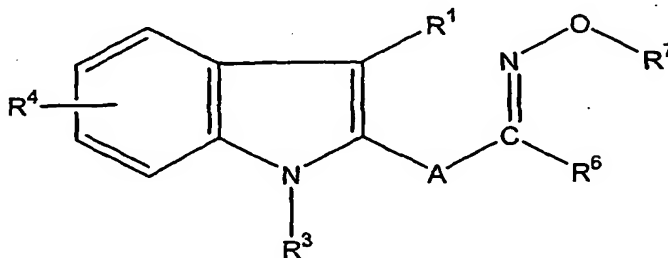


or a pharmaceutically acceptable salt thereof, wherein M is selected from the group consisting of hydrogen, and a pharmaceutically acceptable cation;

B is a straight or branched divalent alkylene group of from one to twelve carbon atoms; Z is selected from the group consisting of: (a) furyl, optionally substituted with alkyl of from one to six carbon atoms, or haloalkyl of from one to six carbon atoms, and (b) thienyl, optionally substituted with alkyl of from one to six carbon atoms, or haloalkyl of from one to six carbon atoms; and L is alkylene of from 1-6 carbon atoms; A is phenyl optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, hydroxyalkyl of from one to six carbon atoms, alkoxy of from one to twelve carbon atoms, alkoxyalkoxy in which the two alkoxy portions may each independently contain from one to six carbon atoms, alkylthio of from one to six carbon atoms, hydroxy, halogen, cyano, amino, alkylamino of from one to six carbon atoms, dialkylamino in which the two alkyl groups may independently contain from one to six carbon atoms, alkanoylamino of from two to eight carbon atoms, N-alkanoyl-N-alkylamino in which the alkanoyl is of from two to eight carbon atoms and the alkyl group is of from one to six carbon atoms, alkylaminocarbonyl of from two to eight carbon atoms, dialkylaminocarbonyl in which the two alkyl groups are independently of from

one to six carbon atoms, carboxyl, alkoxycarbonyl of from two to eight carbon atoms, phenyl, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen, phenoxy, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen, or phenylthio, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen. Preferably, the compound is a compound or a pharmaceutically acceptable salt thereof selected from the group consisting of: N-{3-(5-(4-fluorophenylmethyl)fur-2-yl)-3-butyn-2-yl}-N-hydroxyurea; N-{3-(5-(4-fluorophenylmethyl)-2-thienyl)-1-methyl-2-propynyl}-N-hydroxyurea; (R)-N-{3-(5-(4-fluorophenylmethyl)-2-thienyl)-1-methyl-2-propynyl}-N-hydroxyurea; and (R)-N-{3-(5-(4-chlorophenylmethyl)-2-thienyl)-1-methyl-2-propynyl}-N-hydroxyurea; (S)-N-{3-[5-(4-fluorophenylmethyl)-2-thienyl]-1-methyl-2-propynyl}-N-hydroxyurea. See U.S. Patent No. 5,288,751, incorporated by reference herein.

The compound can be represented by the formula:



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or a pharmaceutically acceptable salt thereof, wherein A is selected from the group consisting of straight or branched divalent alkylene of one to twelve carbon atoms, straight or branched divalent alkenylene of two to twelve carbon atoms, and divalent cycloalkylene of three to eight carbon atoms; R¹ is alkylthio of one to six

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-37-

carbon atoms; R⁶ is selected from the group consisting of hydrogen and alkyl of one to six carbon atoms; R⁷ is selected from the group consisting of (carboxyl)alkyl in which the alkyl portion is of one to six carbon atoms, (alkoxycarbonyl)alkyl in which the alkoxycarbonyl portion is of two to six carbon atoms and the alkyl portion is of one to six carbon atoms, (aminocarbonyl)alkyl in which the alkyl portion is of one to six carbon atoms, ((alkylamino)carbonyl)alkyl in which each alkyl portion independently is of one to six carbon atoms, and ((dialkylamino)carbonyl)alkyl in which each alkyl portion independently is of one to six carbon atoms; R³ is phenylalkyl in which the alkyl portion is of one to six carbon atoms; R⁴ is 2-, 3- or 6-quinolylmethoxy, optionally substituted with alkyl of one to six carbon atoms, haloalkyl of one to six carbon atoms, alkoxy of one to twelve carbon atoms, halogen, or hydroxy. Preferably the compound is selected from the group consisting of: 3-(3-(1,1-dimethylethylthio)-5-(quinolin-2-ylmethoxy)-1-(4-chlorophenylmethyl)-indol-2-yl)-2,2-dimethylpropionaldehyde oxime-O-2 acetic acid; 3-(3-(1,1-dimethylethylthio)-5-(quinolin-2-ylmethoxy)-1-(4-chloro-phenylmethyl) indol-2-yl)-2,2-dimethylpropionaldehyde oxime-O-2-(3-methyl)butyric acid; 3-(3-(1,1-dimethylethylthio)-5-(6,7-dichloroquinolin-2-ylmethoxy)-1-(4-chlorophenylmethyl) indol-2-yl)-2,2-dimethylpropionaldehyde oxime-O-2-acetic acid; and 3-(3-(1,1-dimethylethylthio)-5-(6-fluoroquinolin-2-ylmethoxy)-1-(4chlorophenylmethyl) indol-2-yl)-2,2-dimethylpropionaldehyde oxime-O-2-propionic acid; or a pharmaceutically acceptable salt or ester thereof. See U.S. Patent No. 5,459,150, incorporated by reference herein.

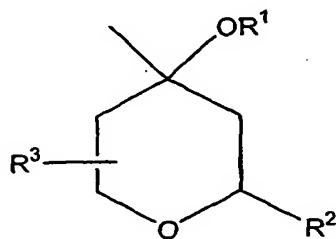
The compound can be represented by the formula:



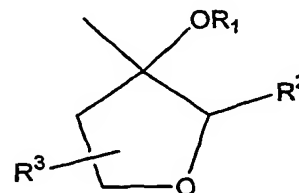
or pharmaceutically acceptable salts thereof, wherein Q is a 9-, 10- or 11-membered bicyclic heterocyclic moiety containing one or two nitrogen heteroatoms and optionally containing a further heteroatom selected from nitrogen, oxygen and sulphur, and Q may optionally bear up to four substituents selected from halogeno, hydroxy, cyano, formyl, oxo, thioxo, (1-4C)alkyl, (3-

4C)alkenyl, (3-4C)alkynyl, (1-4C)alkoxy, fluoro-(1-4C)alkyl, hydroxy-(1-4C)alkyl, (2-5C)alkanoyl, phenyl, benzoyl and benzyl, and wherein said phenyl, benzoyl and benzyl substituents may optionally bear one or two substituents selected from halogeno, (1-4C)alkyl and (1-4C)alkoxy;

- 5 X is oxy, thio, sulphanyl or sulphonyl; Ar is phenylene, pyridinediyl, pyrimidinediyl, thiophenediyl, furandiyl, thiazolediyl, oxazolediyl, thiadiazolediyl or oxadiazolediyl which may optionally bear one or two substituents selected from halogeno, cyano, trifluoromethyl, hydroxy, amino, (1-4C)alkyl, (1-4C)alkoxy, (1-4C)alkylamino and di-(1-4C)alkylamino; and Q is selected from the groups of the
- 10 formulae II and III:



II



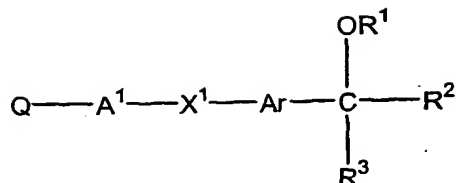
III

- wherein R is hydrogen, (2-5C)alkanoyl or benzoyl, and wherein said benzoyl
- 15 group may optionally bear one or two substituents selected from halogeno, (1-4C)alkyl and (1-4C)alkoxy; R is (1-4C)alkyl; and R is hydrogen or (1-4C)alkyl; or R and R are linked to form a methylene, vinylene, ethylene or trimethylene group. Preferably, the compound is selected from the group consisting of: (2S,4R)-4-[5-fluoro-3-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)phenyl]-4-hydroxy-
- 20 2-ethyltetrahydropyran, (2S,4R)-4-[5-fluoro-3-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylsulphonyl)phenyl]-4-hydroxy-2-methyltetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thiazol-5-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylsulphonyl)thiazol-5-yl]tetrahydropyran,
- 25 (2S,4R)-4-[2-(7-fluoro-1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-

ylthio)thiazol-5-yl]-4-hydroxy-2-methyltetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxoindolin-5-ylthio)thiazol-5-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thien-4-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylsulphonyl)thien-4-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thien-5-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2-dihydroquinolin-6-ylthio)thien-4-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1,8-dimethyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thien-4-yl]tetrahydropyran, 4-[2-(8-fluoro-1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thien-4-yl]-4-hydroxy-2-methyltetrahydropyran, 4-[2-(7-fluoro-1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thien-4-yl]-4-hydroxy-2-methyltetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxoindolin-5-ylthio)thien-4-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[3-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)phenyl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[3-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylsulphonyl)phenyl]tetrahydropyran, (2S,4R)-4-[3-(1-ethyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)phenyl]-4-hydroxy-2-methyltetrahydropyran, (2S,4R)-4-[3-(7-fluoro-1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)phenyl]-4-hydroxy-2-methyltetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[3-(1-methyl-2-oxo-1,2-dihydroquinolin-6-ylthio)phenyl]tetrahydropyran, (2S,4R)-4-[3-(8-chloro-1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)phenyl]-4-hydroxy-2-methyltetrahydropyran and (2S,4R)-4-hydroxy-2-methyl-4-[3-(1-methyl-2-oxoindolin-5-ylthio)phenyl]tetrahydropyran. See EP 623614 B1, incorporated herein by reference.

The compound can be represented by the formula:

-40-



wherein Q is a 10-membered bicyclic heterocyclic moiety containing one or two nitrogen heteroatoms which bears one or two thioxo substituents, and which heterocyclic moiety may optionally bear one, two or three further substituents selected from halogeno, hydroxy, cyano, amino, (1-4C)alkyl, (1-4C)alkoxy, fluoro-(1-4C)alkyl, (1-4C)alkylamino, di-[(1-4C)alkyl]amino, amino-(1-4C)alkyl, (1-4C)alkylamino-(1-4C)alkyl, di-[(1-4C)alkyl]amino-(1-4C)alkyl, phenyl and phenyl-(1-4C)alkyl, and wherein said phenyl or phenyl-(1-4C)alkyl substituent may optionally bear a substituent selected from halogeno, (1-4C)alkyl and (1-4C)alkoxy;

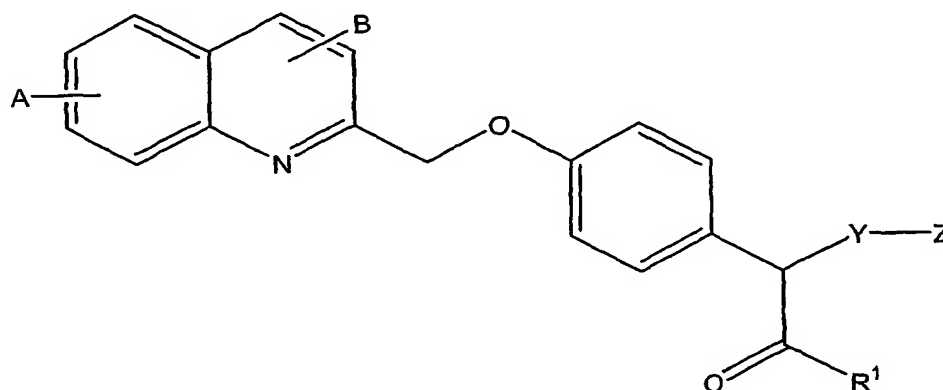
wherein A is a direct link to X or is (1-3C)alkylene; wherein X is oxy, thio, sulphinyl, sulphonyl or imino; wherein Ar is phenylene which may optionally bear one or two substituents selected from halogeno, hydroxy, amino, nitro, cyano, carbamoyl, ureido, (1-4C)alkyl, (1-4C)alkoxy, (1-4C)alkylamino, di-[(1-4C)alkyl]amino, fluoro-(1-4C)alkyl and (2-4C)alkanoylamino; or Ar is pyridylene; wherein R is (1-4C)alkyl, (3-4C)alkenyl or (3-4C)alkynyl; and wherein R and R together form a group of the formula -A-X-A- which, together with the carbon atom to which A and A are attached, defines a ring having 5 to 7 ring atoms, wherein A and A, which may be the same or different, each is (1-3C)alkylene and X is oxy, thio, sulphinyl or sulphonyl, and which ring may bear one, two or three substituents, which may be the same or different, selected from hydroxy, (1-4C)alkyl and (1-4C)alkoxy; or wherein R and R together form a group of the formula -A-X-A- which, together with the oxygen atom to which A is attached and with the carbon atom to which A is attached, defines a ring having 5 to 7 ring atoms, wherein A and A, which may be the same or different, each is (1-3C)alkylene and X is oxy, thio, sulphinyl or sulphonyl, and which ring may bear

-41-

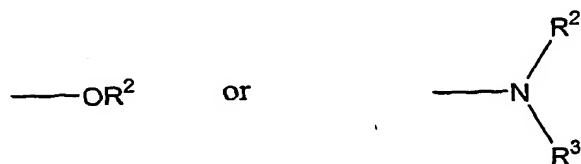
one, two or three (1-4C)alkyl substituents, and wherein R is (1-4C)alkyl, (2-4C)alkenyl or (2-4C)alkynyl; or a pharmaceutically-acceptable salt thereof.

Preferably, the compound is selected from the group consisting of: 4-(5-fluoro-3-(1-methyl-2-thioxo-1,2-dihydroquinolin-6-ylmethoxy)phenyl]-4-ethoxytetrahydropyran and 4-(5-fluoro-3-(1-methyl-2-thioxo-1,2,3,4-tetrahydroquinolin-6-ylmethoxy)phenyl]-4-methoxytetrahydropyran, 4-(5-fluoro-3-(1-methyl-2-thioxo-1,2,3,4-tetrahydroquinolin-6-ylthio)phenyl]-4-methoxytetrahydropyran and pharmaceutically-acceptable salt thereof. See EP 466452 B1, incorporated herein by reference.

The compound can be a substituted 4-(quinolin-2-ylmethoxy)phenylacetic acid derivative represented by the following formula:

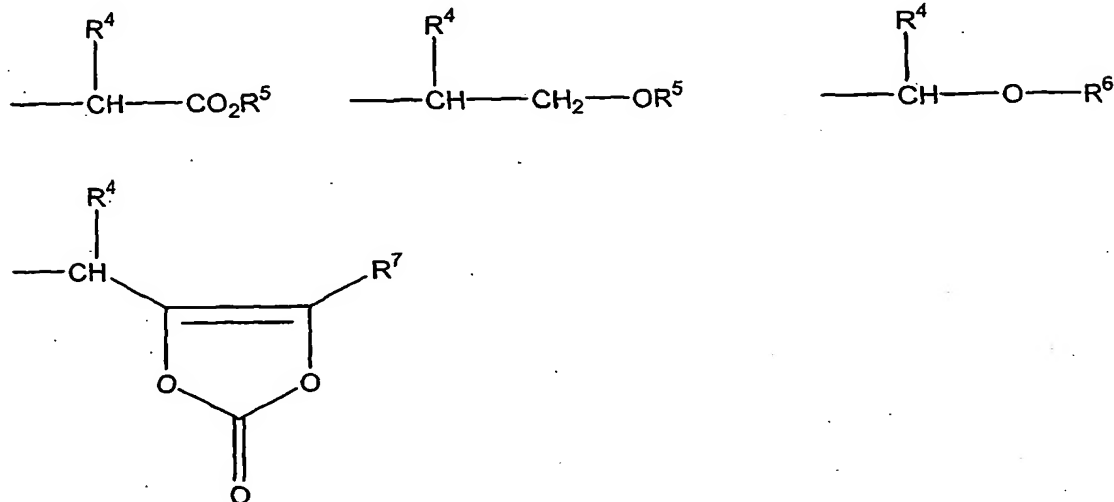


or pharmaceutically acceptable salt thereof, wherein R^1 represents a group of the formula:



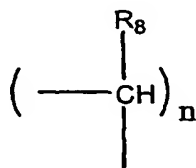
-42-

R^2 and R^3 are identical or different and represent hydrogen, lower alkyl, phenyl, benzyl or a group of the formula:



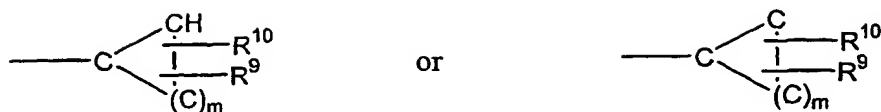
10 R^4 represents hydrogen, lower alkyl, phenyl or benzyl, which can optionally be substituted by hydroxyl, carboxyl, lower alkoxy, carbonyl, lower alkylthio, heteroaryl or carbamoyl, R^5 represents hydrogen, lower alkyl, phenyl or benzyl, R^6 represents a group of the formula $-\text{COR}^5$ or $-\text{CO}^2R^5$, R^7 represents hydrogen, lower alkyl or phenyl, Y represents a group of the formula:

15



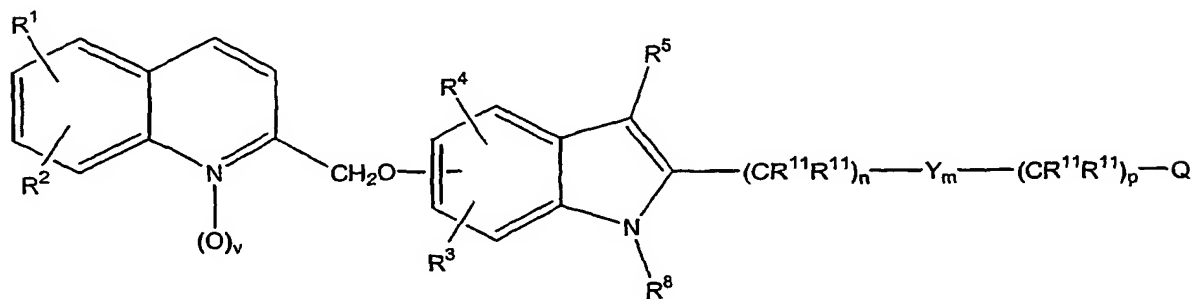
20 wherein R^8 represents hydrogen, lower alkyl or phenyl and n denotes a number of 0 to 5, Z represents norbornyl, or represents a group of the formula:

-43-



wherein R^9 and R^{10} are identical or different and denote hydrogen, lower alkyl or phenyl, or R^9 and R^{10} can together form a saturated carbocyclic ring having up to 6 carbon atoms and m denotes a number from 1 to 6, and A and B are identical or different and denote hydrogen, lower alkyl or halogen, or a pharmaceutically acceptable salt thereof. Preferably the compounds are selected from the group consisting of: 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cyclopentylacetic acid, 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cyclohexylacetic acid, and 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cycloheptylacetic acid, (+)-enantiomer of 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cyclopentylacetic acid, (-)-enantiomer of 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cyclopentylacetic acid and pharmaceutically acceptable salts thereof. See U.S. Patent No. 4,970,215, incorporated herein by reference.

The compound can be represented by the formula:



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wherein R, R, R, R and R are independently hydrogen, halogen, lower alkyl, lower alkenyl, lower alkynyl, $-\text{CF}_3$, $-\text{CN}$, $-\text{NO}_2$, $-\text{N}_3$, $-\text{C}(\text{OH})\text{RR}$, $-\text{CO}_2\text{R}$, $-\text{SR}$, $-\text{S}(\text{O})\text{R}$, $-\text{S}(\text{O})_2\text{R}$, $-\text{S}(\text{O})_2\text{NRR}$, $-\text{OR}$, $-\text{NRR}$, $-\text{C}(\text{O})\text{R}$ or $-(\text{CH}_2)_t\text{R}$; R is hydrogen,

-CH₃, -CF₃, -C(O)H, X-R or X-R; R and R are independently: alkyl, -
 (CH₂)_uPh(R)₂ or -(CH₂)_uTh(R)₂; R is -CF₃ or R; R is hydrogen or X-R; each R
 is independently hydrogen or lower alkyl, or two R's on same carbon atom are
 joined to form a cycloalkyl ring of 3 to 6 carbon atoms; R is hydrogen, lower alkyl
 5 or -CH₂R;

R is lower alkyl or -(CH₂)_rR; R is -CF₃ or R; R is hydrogen, -C(O)R, R, or two R
 's on the same nitrogen may be joined to form a monocyclic heterocyclic ring of 4
 to 6 atoms containing up to 2 heteroatoms chosen from O, S or N; R is hydrogen, -
 CF₃, lower alkyl, lower alkenyl, lower alkynyl or -(CH₂)_rR; R is -(CH₂)_s-C(RR)-
 10 (CH₂)_s-R or -CH₂C(O)NRR; R is hydrogen or lower alkyl; R is a) a monocyclic
 or bicyclic heterocyclic ring containing from 3 to 9 nuclear carbon atoms and 1 or
 2 nuclear hetero-atoms selected from N, S or O and with each ring in the
 heterocyclic radical being formed of 5 or 6 atoms, or b) the radical W-R; R is
 alkyl or C(O)R;

15 R is phenyl substituted with 1 or 2 R groups; R is hydrogen, halogen, lower alkyl,
 lower alkoxy, lower alkylthio, lower alkylsulfonyl, lower alkylcarbonyl, -CF₃, -
 CN,

-NO₂ or -N₃; R is alkyl, cycloalkyl, monocyclic monoheterocyclic ring;

R is the residual structure of a standard amino acid, or R and R attached to the

20 same N can cyclize to form a proline residue; m is 0 to 1; n is 0 to 3; p is 1 to 3

when m is 1; p is 0 to 3 when m is 0; r is 0 to 2; s is 0 to 3; t is 0 to 2; u is 0 to 3; v
 is 0 or 1;

W is O, S or NR; X is O, or NR; X is C(O), CRR, S, S(O) or S(O)₂; X is C(O),

CRR, S(O)₂ or a bond; Y is X or X; Q is -CO₂R, -C(O)NHS(O)₂R, -NHS(O)₂R,

25 -S(O)₂NHR -C(O)NRR, -CO₂R, -C(O)NRR, -CH₂OH, or 1H- or 2H-tetrazol-5-
 yl;

and the pharmaceutically acceptable salts thereof. Preferred embodiments of the
 compounds are selected from the following and pharmaceutically acceptable salts
 thereof:

- 3-[N-(p-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-ylmethoxy)indol-2-yl]-
2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-methyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-
2,2-dimethylpropanoic acid;
- 5 3-[N-(p-t-butylthiobenzyl)-3-(t-butylthio)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-(phenylthio)-5-(quinolin-2-ylmethoxy)indol-
2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-(phenylsulfonyl)-5-(quinolin-2-
10 ylmethoxy)indol-2-yl]-2,2-dimethyl propanoic acid, N-oxide;
- 3-[N-(p-chlorobenzyl)-3-(phenylsulfonyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-(phenylsulfinyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 15 3-[N-(p-chlorobenzyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-
dimethylpropanoic acid;;
- 3-[N-(p-chlorobenzyl)-3-benzoyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-
2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-benzyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-
2,2-dimethylpropanoic acid;
- 20 3-[N-(p-chlorobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 2-[N-(p-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-ylmethoxy)indol-
2-yl]ethoxyethanoic acid;
- 25 3-[N-(p-chlorobenzyl)-3-(3,3-dimethyl-1-butyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-ylmethoxy)indol-
2-yl]-2-methylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-methyl-5-(6,7-dichloroquinolin-2-
30 ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-methyl-5-(7-chloroquinolin-2-

- ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
3-[N-(p-chlorobenzyl)-4-allyl-5-(quinolin-2-ylmethoxy)-3-(t-butylthio)indol-2-yl]-2,2-dimethylpropanoic acid;
3-[N-(p-chlorobenzyl)-4-allyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-
5 2,2-dimethylpropanoic acid;
3-[N-(p-chlorobenzyl)-6-(quinolin-2-ylmethoxy)-3-(t-butylthio)indol-2-yl]-2,2-dimethylpropanoic acid;
3-[N-(p-chlorobenzyl)-4-(quinolin-2-ylmethoxy)-3-(t-butylthio)indol-2-yl]-2,2-dimethylpropanoic acid;
10 3-[N-(p-chlorobenzyl)-7-(quinolin-2-ylmethoxy)-3-(t-butylthio)indol-2-yl]-2,2-dimethylpropanoic acid;
2-[2-[N-(p-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-ylmethoxy)indol-2-yl]ethoxy]propanoic acid;
3-[N-(p-chlorobenzyl)-4-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-
15 dimethylpropanoic acid;;
3-[N-methyl-3-(p-chlorobenzoyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-methyl-3-(p-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-
2,2-dimethylpropanoic acid,
20 3-[N-(4-chlorobenzyl)-3-i-propoxy-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-yl-methoxy)indol-2-yl]-2-ethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-trifluoroacetyl-5-(quinolin-2-
25 ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2-methylpropanoic acid,
3-[3-(3,3-dimethyl-1-oxo-1-butyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
30 3-[N-(4-triflouromethylbenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-yl-methoxy)indol-2-yl]-2,2-dimethylpropanoic acid,

- 3-[N-benzyl-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-(3-methoxybenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 5 3-[N-allyl-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-(4-methoxybenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-methyl-3-(3,3-dimethyl-1-oxo-3-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 10 3-[3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid.
- 3-[N-(phenylsulfonyl)-3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 15 3-[N-benzyl-3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-(4-chlorobenzyl)-3-(t-butylsulfonyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-(4-chlorobenzyl)-3-(t-butylsulfinyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 20 3-[N-allyl-3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-(n-propyl)-3-(4-chlorobenzyl)-6-(quinoline-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 25 3-[N-ethyl-3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-(4-chlorobenzyl)-3-(4-t-butylbenzoyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-(4-chlorobenzyl)-3-(4-chlorobenzoyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 30 3-[N-(4-chlorobenzyl)-3-(1,1-dimethylethyl)-5-(quinolin-2-

- ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-acetyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-
2,2-dimethylpropanoic acid
3-[N-(4-chlorobenzyl)-3-cyclopropanecarbonyl-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
5 3-[N-(4-chlorobenzyl)-3-(3-cyclopentylpropanoyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(3-methylbutanoyl)-5-(quinolin-2-yl-
methoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
10 3-[N-(4-chlorobenzyl)-3-propanoyl-5-(quinolin-2-ylmethoxy)indol-2-
yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(2-methylpropanoyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-trimethylacetyl-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
15 3-[N-(4-chlorobenzyl)-3-phenylacetyl-5-(quinolin-2-ylmethoxy)indol-
2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-fluorobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
20 3-[N-(4-bromobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-iodobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(1,1-dimethylbutyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
25 3-[N-(4-chlorobenzyl)-3-(1,1-dimethylpropyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(3-fluorobenzyl)-3-(1,1-dimethylethyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
30 3-[N-(4-chlorobenzyl)-3-(3-methylethyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,

- 3-[N-(4-chlorobenzyl)-3-cyclopropyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-(1-methyl-1-cyclopropyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 5 3-[N-(4-chlorobenzyl)-3-cyclopentyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-cyclohexyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-(α , α -dimethylbenzyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 10 3-[N-(4-chlorobenzyl)-3-(2-{4-chloro- α , α -dimethylbenzyl})-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-(1-adamantyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 15 3-[N-(4-chlorobenzyl)-3-((1-adamantyl)methyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(1,1-dimethylethyl)-3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(1,1-dimethylpropyl)-3-(4-chlorobenzyl)-6-(quinoline-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 20 3-[N-(4-chlorobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-diethylpropanoic acid,
 methyl 3-[N-(4-chlorobenzyl)-3,6-bis(acetyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2 dimethyl propanoate or
 25 methyl 3-[N-(4-chlorobenzyl)-3,6-bis(cyclopropanecarbonyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethyl propanoate. See EP 419049 B1, incorporated herein by reference.

The term "alkyl" refers to a monovalent group derived from a straight or branched chain saturated hydrocarbon by the removal of a single hydrogen
 30 atom. Alkyl groups are exemplified by methyl, ethyl, n- and iso-propyl, n-, sec-, iso- and tert-butyl, and the like. The term "hydroxyalkyl" represents an

alkyl group, as defined above, substituted by one to three hydroxyl groups with the proviso that no more than one hydroxy group may be attached to a single carbon atom of the alkyl group. The term "alkylamino" refers to a group having the structure -NHR' wherein R' is alkyl, as previously defined, examples of alkylamino include methylamino, ethylamino, iso-propylamino and the like. The term "alkylaminocarbonyl" refers to an alkylamino group, as previously defined, attached to the parent molecular moiety through a carbonyl group. Examples of alkylaminocarbonyl include methylaminocarbonyl, ethylaminocarbonyl, iso-propylaminocarbonyl and the like. The term "alkylthio" refers to an alkyl group, as defined above, attached to the parent molecular moiety through a sulfur atom and includes such examples as methylthio, ethylthio, propylthio, n-, sec- and tert-butylthio and the like. The term "alkanoyl" represents an alkyl group, as defined above, attached to the parent molecular moiety through a carbonyl group. Alkanoyl groups are exemplified by formyl, acetyl, propionyl, butanoyl and the like. The term "alkanoylamino" refers to an alkanoyl group, as previously defined, attached to the parent molecular moiety through a nitrogen atom. Examples of alkanoylamino include formamido, acetamido, and the like. The term "N-alkanoyl-N-alkylamino" refers to an alkanoyl group, as previously defined, attached to the parent molecular moiety through an aminoalkyl group. Examples of N-alkanoyl-N-alkylamino include N-methylformamido, N-methyl-acetamido, and the like. The terms "alkoxy" or "alkoxyl" denote an alkyl group, as defined above, attached to the parent molecular moiety through an oxygen atom. Representative alkoxy groups include methoxyl, ethoxyl, propoxyl, butoxyl, and the like. The term "alkoxyalkoxyl" refers to an alkyl group, as defined above, attached through an oxygen to an alkyl group, as defined above, attached in turn through an oxygen to the parent molecular moiety. Examples of alkoxyalkoxyl include methoxymethoxyl, methoxyethoxyl, ethoxyethoxyl and the like. The term "alkoxyalkyl" refers to an alkoxy group, as defined above, attached through an alkylene group to the parent molecular moiety. The term "alkoxycarbonyl" represents an ester

group; *i.e.*, an alkoxy group, attached to the parent molecular moiety through a carbonyl group such as methoxycarbonyl, ethoxycarbonyl, and the like. The term "alkenyl" denotes a monovalent group derived from a hydrocarbon containing at least one carbon-carbon double bond by the removal of a single hydrogen atom. Alkenyl groups include, for example, ethenyl, propenyl, butenyl, 1-methyl-2-buten-1-yl and the like. The term "alkylene" denotes a divalent group derived from a straight or branched chain saturated hydrocarbon by the removal of two hydrogen atoms, for example methylene, 1,2-ethylene, 1,1-ethylene, 1,3-propylene, 2,2-dimethylpropylene, and the like. The term "alkenylene" denotes a divalent group derived from a straight or branched chain hydrocarbon containing at least one carbon-carbon double bond. Examples of alkenylene include $-\text{CH}=\text{CH}-$, $-\text{CH}_2\text{CH}=\text{CH}-$, $-\text{C}(\text{CH}_3)=\text{CH}-$, $-\text{CH}_2\text{CH}=\text{CHCH}_2-$, and the like. The term "cycloalkylene" refers to a divalent group derived from a saturated carbocyclic hydrocarbon by the removal of two hydrogen atoms, for example cyclopentylene, cyclohexylene, and the like. The term "cycloalkyl" denotes a monovalent group derived from a monocyclic or bicyclic saturated carbocyclic ring compound by the removal of a single hydrogen atom. Examples include cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, bicyclo[2.2.1]heptanyl, and bicyclo[2.2.2]octanyl. The term "alkynylene" refers to a divalent group derived by the removal of two hydrogen atoms from a straight or branched chain acyclic hydrocarbon group containing a carbon-carbon triple bond. Examples of alkynylene include $-\text{CH}\equiv\text{CH}-$, $-\text{CH}\equiv\text{CH}-\text{CH}_2-$, $-\text{CH}\equiv\text{CH}-\text{CH}(\text{CH}_3)-$, and the like. The term "carbocyclic aryl" denotes a monovalent carbocyclic ring group derived by the removal of a single hydrogen atom from a monocyclic or bicyclic fused or non-fused ring system obeying the " $4n+2$ p electron" or Huckel aromaticity rule. Examples of carbocyclic aryl groups include phenyl, 1- and 2-naphthyl, biphenyl, fluorenyl, and the like. The term "(carbocyclic aryl)alkyl" refers to a carbocyclic aryl ring group as defined above, attached to the parent molecular moiety through an alkylene group. Representative (carbocyclic aryl)alkyl groups include phenylmethyl,

phenylethyl, phenylpropyl, 1-naphthylmethyl, and the like. The term "carbocyclicarylalkoxy" refers to a carbocyclicaryl alkyl group, as defined above, attached to the parent molecular moiety through an oxygen atom. The term "carbocyclic aryloxyalkyl" refers to a carbocyclic aryl group, as defined
5 above, attached to the parent molecular moiety through an oxygen atom and thence through an alkylene group. Such groups are exemplified by phenoxymethyl, 1- and 2-naphthyloxymethyl, phenoxyethyl and the like. The term "(carbocyclic aryl)alkoxyalkyl" denotes a carbocyclic aryl group as defined above, attached to the parent molecular moiety through an alkoxyalkyl
10 group. Representative (carbocyclic aryl)alkoxyalkyl groups include phenylmethoxymethyl, phenylethoxymethyl, 1- and 2-naphthylmethoxyethyl, and the like. "Carbocyclic arylthioalkyl" represents a carbocyclic aryl group as defined above, attached to the parent molecular moiety through a sulfur atom and thence through an alkylene group and are typified by
15 phenylthiomethyl, 1- and 2-naphthylthioethyl and the like. The term "dialkylamino" refers to a group having the structure -NR'R" wherein R' and R" are independently selected from alkyl, as previously defined. Additionally, R' and R" taken together may optionally be $-(CH_2)_{kk}-$ where kk is an integer of from 2 to 6. Examples of dialkylamino include, dimethylamino,
20 diethylaminocarbonyl, methylethylamino, piperidino, and the like. The term "halo or halogen" denotes fluorine, chlorine, bromine or iodine. The term "haloalkyl" denotes an alkyl group, as defined above, having one, two, or three halogen atoms attached thereto and is exemplified by such groups as chloromethyl, bromoethyl, trifluoromethyl, and the like. The term
25 "hydroxyalkyl" represents an alkyl group, as defined above, substituted by one to three hydroxyl groups with the proviso that no more than one hydroxy group may be attached to a single carbon atom of the alkyl group. The term "phenoxy" refers to a phenyl group attached to the parent molecular moiety through an oxygen atom. The term "phenylthio" refers to a phenyl group
30 attached to the parent molecular moiety through a sulfur atom. The term "pyridyloxy" refers to a pyridyl group attached to the parent molecular moiety

through an oxygen atom. The terms "heteroaryl" or "heterocyclic aryl" as used herein refers to substituted or unsubstituted 5- or 6-membered ring aromatic groups containing one oxygen atom, one, two, three, or four nitrogen atoms, one nitrogen and one sulfur atom, or one nitrogen and one oxygen atom. The term heteroaryl also includes bi-or tricyclic groups in which the aromatic heterocyclic ring is fused to one or two benzene rings. Representative heteroaryl groups are pyridyl, thienyl, indolyl, pyrazinyl, isoquinolyl, pyrrolyl, pyrimidyl, benzothienyl, furyl, benzo[b]furyl, imidazolyl, thiazolyl, carbazolyl, and the like. The term "heteroarylalkyl" denotes a heteroaryl group, as defined above, attached to the parent molecular moiety through an alkylene group. The term "heteroaryloxy" denotes a heteroaryl group, as defined above, attached to the parent molecular moiety through an oxygen atom. The term "heteroarylalkoxy" denotes a heteroarylalkyl group, as defined above, attached to the parent molecular moiety through an oxygen atom.

NUCLEIC ACID THERAPEUTIC AGENTS

In another embodiment, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (*e.g.*, an oligonucleotide as described below); or a nucleic acid encoding a member of the leukotriene pathway (*e.g.*, 5-LO), can be used in "antisense" therapy, in which a nucleic acid (*e.g.*, an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a nucleic acid is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the polypeptide encoded by that mRNA and/or DNA, *e.g.*, by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it

produces RNA that is complementary to a portion of the mRNA and/or DNA that encodes the polypeptide for the member of the leukotriene pathway (*e.g.*, FLAP or 5-LO). Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the polypeptide. In one embodiment, the oligonucleotide probes are modified oligonucleotides that are resistant to endogenous nucleases, *e.g.*, exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Pat. Nos. 5,176,996, 5,264,564 and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.* (*Biotechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the polypeptide. The antisense oligonucleotides bind to mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

5 The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.* for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication No. 10 WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication No. WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *BioTechniques* 6:958-976 (1988)) or intercalating agents. (See, *e.g.*, Zon, *Pharm.Res.* 5: 539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, 15 hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

The antisense molecules are delivered to cells that express the member of the leukotriene pathway *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be 20 injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use 25 of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous transcripts and thereby prevent translation of the mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense 30 RNA. Such a vector can remain episomal or become chromosomally

integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically).

In another embodiment of the invention, small double-stranded interfering RNA (RNA interference (RNAi)) can be used. RNAi is a post-transcription process, in which double-stranded RNA is introduced, and sequence-specific gene silencing results, through catalytic degradation of the targeted mRNA. See, *e.g.*, Elbashir, S.M. *et al.*, *Nature* 411:494-498 (2001); Lee, N.S., *Nature Biotech.* 19:500-505 (2002); Lee, S-K. *et al.*, *Nature Medicine* 8(7):681-686 (2002); the entire teachings of these references are incorporated herein by reference.

Endogenous expression of a member of the leukotriene pathway (*e.g.*, FLAP, 5-LO) can also be reduced by inactivating or "knocking out" the gene or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, an altered, non-functional gene of a member of the leukotriene pathway (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous gene (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the gene *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the gene. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above. Alternatively, expression of non-altered genes can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-altered functional gene, or the complement

thereof, or a portion thereof, in place of an gene in the cell, as described above. In another embodiment, targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a polypeptide variant that differs from that present in the cell.

5 Alternatively, endogenous expression of a member of the leukotriene pathway can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the member of the leukotriene pathway (*i.e.*, the promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells in the body. (See
10 generally, Helene, C., *Anticancer Drug Des.*, 6(6):569-84 (1991); Helene, C. *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity of one of the members of the leukotriene pathway, can be used in the manipulation of tissue, *e.g.*, tissue
15 differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a nucleic acid RNA or nucleic acid sequence) can be used to investigate the role of one or more members of the leukotriene pathway in the development of
20 disease-related conditions. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

 The therapeutic agents as described herein can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic agents
25 can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Pat. No. 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein. In addition, a
30 combination of any of the above methods of treatment (*e.g.*, administration of non-altered polypeptide in conjunction with antisense therapy targeting altered mRNA for a member of the leukotriene pathway; administration of a first

splicing variant in conjunction with antisense therapy targeting a second splicing variant) can also be used.

The invention additionally pertains to use of such therapeutic agents, as described herein, for the manufacture of a medicament for the treatment of MI, ACS, and/or atherosclerosis, e.g., using the methods described herein.

MONITORING PROGRESS OF TREATMENT

The current invention also pertains to methods of monitoring the response of an individual, such as an individual in one of the target populations described above, to treatment with a leukotriene synthesis inhibitor. Because the level of inflammatory markers can be elevated in individuals who are in the target populations described above, an assessment of the level of inflammatory markers of the individual both before, and during, treatment with the leukotriene synthesis inhibitor will indicate whether the treatment has successfully decreased production of leukotrienes in the arterial vessel wall or in bone-marrow derived inflammatory cells.

For example, in one embodiment of the invention, an individual who is a member of a target population of individuals at risk for MI or ACS (*e.g.*, an individual in a target population described above, such as an individual at-risk due to a FLAP MI-haplotype) can be assessed for response to treatment with a leukotriene synthesis inhibitor, by examining leukotriene levels in the individual. Serum, plasma or urinary leukotrienes (*e.g.*, leukotriene E4, cysteinyl leukotriene 1), or *ex vivo* production of leukotrienes (*e.g.*, in blood samples stimulated with a calcium ionophore to produce leukotrienes) can be measured before, and during or after treatment with the leukotriene synthesis inhibitor. The leukotriene level before treatment is compared with the leukotriene level during or after treatment. The efficacy of treatment is indicated by a decrease in leukotriene production: a level of leukotriene during or after treatment that is significantly lower than the level of leukotriene before treatment, is indicative of efficacy. A level that is lower during or after treatment can be shown, for example, by decreased serum or

urinary leukotrienes, or decreased *ex vivo* production of leukotrienes. A level that is "significantly lower", as used herein, is a level that is less than the amount that is typically found in control individual(s), or is less in a comparison of disease risk in a population associated with the other bands of measurement (e.g., the mean or median, the highest quartile or the highest quintile) compared to lower bands of measurement (e.g., the mean or median, the other quartiles; the other quintiles).

In another embodiment of the invention, an individual who is a member of a target population of individuals at risk for MI or ACS (e.g., an individual in a target population described above, such as an individual at-risk due to elevated C-reactive protein) can be assessed for response to treatment with a leukotriene synthesis inhibitor, by examining levels of inflammatory markers in the individual. For example, levels of an inflammatory marker in an appropriate test sample (e.g., serum, plasma or urine) can be measured before, and during or after treatment with the leukotriene synthesis inhibitor. The level of the inflammatory marker before treatment is compared with the level of the inflammatory marker during or after treatment. The efficacy of treatment is indicated by a decrease in the level of the inflammatory marker, that is, a level of the inflammatory marker during or after treatment that is significantly lower (e.g., significantly lower), than the level of inflammatory marker before treatment, is indicative of efficacy. Representative inflammatory markers include: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite (e.g., cysteinyl leukotriene 1), interleukin-6, tissue necrosis factor-alpha, soluble vascular cell adhesion molecules (sVCAM), soluble intervascular adhesion molecules (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9. In a preferred embodiment, the marker is CRP.

PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising agents described herein, for example, an agent that is a leukotriene synthesis inhibitor as described herein. For instance, a leukotriene synthesis inhibitor can be formulated with a physiologically acceptable carrier or excipient to prepare a pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrrolidone, etc., as well as combinations thereof. The pharmaceutical preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, polyvinyl pyrrolidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of

introduction can also include gene therapy (as described below), rechargeable or biodegradable devices, particle acceleration devices ("gene guns") and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

5 The composition can be formulated in accordance with the routine procedures as a pharmaceutical composition adapted for administration to human beings. For example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic to
10 ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed
15 with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

 For topical application, nonsprayable forms, viscous to semi-solid or
20 solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, enemas, lotions, sols, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary
25 agents, *e.g.*, preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze bottle or
30 in admixture with a pressurized volatile, normally gaseous propellant, *e.g.*, pressurized air.

Agents described herein can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those
5 derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or
10 condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms, and should be decided according to the judgment of a practitioner and each
15 patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with
20 such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug
25 administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet.
30 Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is intended to mean a dosage that is

dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

NUCLEIC ACIDS OF THE INVENTION

5 *FLAP Nucleic Acids, Portions and Variants*

In addition, the invention pertains to isolated nucleic acid molecules comprising a human FLAP nucleic acid. The term, "FLAP nucleic acid," as used herein, refers to an isolated nucleic acid molecule encoding FLAP
10 polypeptide. The FLAP nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-stranded; single stranded RNA or DNA can be either the coding, or sense strand or the non-coding, or antisense strand. The nucleic acid molecule can include all or a portion of the
15 coding sequence of the gene or nucleic acid and can further comprise additional non-coding sequences such as introns and non-coding 3' and 5' sequences (including regulatory sequences, for example, as well as promoters, transcription enhancement elements, splice donor/acceptor sites, etc.).

For example, a FLAP nucleic acid can consist of SEQ ID NOs: 1 or 3
20 or the complement thereof, or to a portion or fragment of such an isolated nucleic acid molecule (e.g., cDNA or the nucleic acid) that encodes FLAP polypeptide (e.g., a polypeptide such as SEQ ID NO: 2). In a preferred embodiment, the isolated nucleic acid molecule comprises a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1 or 3, or their
25 complement thereof.

Additionally, the nucleic acid molecules of the invention can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those that encode a glutathione-S-transferase (GST)
30 fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleic acid sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (e.g., as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. In certain embodiments, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb, including but not limited to 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention. An isolated nucleic acid molecule or nucleic acid sequence can include a nucleic acid molecule or nucleic acid sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained

in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleotide sequences include recombinant DNA molecules in heterologous organisms, as well as partially or substantially purified DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleotide sequences. Such isolated nucleotide sequences are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (*e.g.*, from other mammalian species), for gene mapping (*e.g.*, by *in situ* hybridization with chromosomes), or for detecting expression of the nucleic acid in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode a FLAP polypeptide (*e.g.*, a polypeptide having an amino acid sequence comprising an amino acid sequence of SEQ ID NOs: 2), or another splicing variant of a FLAP polypeptide or polymorphic variant thereof. Thus, for example, DNA molecules that comprise a sequence that is different from the naturally occurring nucleic acid sequence but which, due to the degeneracy of the genetic code, encode a FLAP polypeptide of the present invention are also the subjects of this invention. The invention also encompasses nucleotide sequences encoding portions (fragments), or encoding variant polypeptides such as analogues or derivatives of a FLAP polypeptide. Such variants can be naturally occurring, such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of a FLAP polypeptide. In one preferred embodiment, the nucleotide sequences are fragments that comprise one or more polymorphic microsatellite markers. In another preferred embodiment,

the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in a FLAP nucleic acid (*e.g.*, the single nucleotide polymorphisms set forth in Table 3, below).

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to a designated sequence via hydrogen bonding and other chemical interactions. Such molecules include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleic acid sequence described herein (*e.g.*, nucleic acid molecules which specifically hybridize to a nucleic acid sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleic acid sequence comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1 or 3 or the complement thereof. In another embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleic acid sequence encoding an amino acid sequence of SEQ ID NO: 2 or a polymorphic variant thereof. In a preferred embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a FLAP.

Such nucleic acid molecules can be detected and/or isolated by specific hybridization (*e.g.*, under high stringency conditions). "Specific

hybridization,” as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (e.g., when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a sample wherein the hybridization is to be performed). “Stringency conditions” for hybridization is a term of art which refers to the incubation and wash conditions, e.g., conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (i.e., 100%) complementary to the second, or the first and second may share some degree of complementarity that is less than perfect (e.g., 70%, 75%, 85%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. “High stringency conditions”, “moderate stringency conditions” and “low stringency conditions” for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. et al., “*Current Protocols in Molecular Biology*”, John Wiley & Sons, (1998), the entire teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (e.g., 0.2X SSC, 0.1X SSC), temperature (e.g., room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 60%, at least about 70%, at least about 80%, at least about 90% or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization

conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*, selectively) with the most similar sequences in the sample can be determined.

5 Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200: 546-556 (1991), and in, Ausubel, *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, (1998), which describes the determination of washing conditions for moderate or low stringency conditions. Washing is the step in which conditions are usually set
10 so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize.
15 Generally, doubling the concentration of SSC results in an increase in T_m of -17°C. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

For example, a low stringency wash can comprise washing in a
20 solution containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate stringency wash can comprise washing in a prewarmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in prewarmed (68°C) solution containing 0.1X SSC/0.1%SDS for 15 minutes at 68°C. Furthermore, washes
25 can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

30 The percent homology or identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal

comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first sequence for optimal alignment). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). When a position in one sequence is occupied by the same nucleotide or amino acid residue as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, nucleic acid or amino acid "homology" is equivalent to nucleic acid or amino acid "identity". In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, for example, at least 40%, in certain embodiments at least 60%, and in other embodiments at least 70%, 80%, 90% or 95% of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA* 90:5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, *CABIOS* 4(1): 11-17 (1988). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (Accelrys, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include

ADVANCE and ADAM as described in Torellis and Robotti, *Comput. Appl. Biosci.* 10:3-5 (1994); and FASTA described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-8 (1988).

5 In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software package using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package using a
10 gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleic acid sequence comprising SEQ ID NO: 1 or 3 or the complement of SEQ ID NO: 1 or 3, and also provides isolated nucleic acid
15 molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleic acid sequence encoding an amino acid sequence of the invention or polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, for example, at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200 or more nucleotides
20 in length. Longer fragments, for example, 30 or more nucleotides in length, encoding antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

Probes and Primers

25 In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers" are oligonucleotides that hybridize in a base-specific manner to a complementary strand of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.* (*Science*
30 254:1497-1500 (1991)).

5 A probe or primer comprises a region of nucleic acid that hybridizes to at least about 15, for example about 20-25, and in certain embodiments about 40, 50 or 75, consecutive nucleotides of a nucleic acid of the invention, such as a nucleic acid comprising a contiguous nucleic acid sequence of SEQ ID
10 NOS: 1 or 3 or the complement of SEQ ID Nos: 1 or 3, or a nucleic acid sequence encoding an amino acid sequence of SEQ ID NO: 2 or polymorphic variant thereof. In preferred embodiments, a probe or primer comprises 100 or fewer nucleotides, in certain embodiments, from 6 to 50 nucleotides, for example, from 12 to 30 nucleotides. In other embodiments, the probe or
15 primer is at least 70% identical to the contiguous nucleic acid sequence or to the complement of the contiguous nucleotide sequence, for example, at least 80% identical, in certain embodiments at least 90% identical, and in other embodiments at least 95% identical, or even capable of selectively hybridizing to the contiguous nucleic acid sequence or to the complement of the
contiguous nucleotide sequence. Often, the probe or primer further comprises a label, e.g., radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology
20 techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated using the polymerase chain reaction and synthetic oligonucleotide primers based on one or more of SEQ ID NOS: 1 or 3, or the complement thereof, or designed based on nucleotides based on sequences encoding one or more of the amino acid
25 sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19:4967 (1991); Eckert *et al.*, *PCR Methods and Applications* 1:17 (1991);
30 PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic

DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), transcription amplification (Kwoh, *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be labeled, for example, radiolabeled, and used as a probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can be obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a polypeptide of the appropriate molecular weight. For example, the direct analysis of the nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of SEQ ID NOs: 1 or 3 and/or the complement of one or more of SEQ ID NOs: 1 or 3 and/or a portion of one or more of SEQ ID NOs: 1 or 3 or the complement of one or more of SEQ ID NOs: 1 or 3 and/or a sequence encoding the amino acid sequences of SEQ ID NOs: 2 or encoding a portion of one or more of SEQ ID NOs: 1 or 3 or their

complement. They can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders related to FLAP, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions or nucleic acid regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or

diagnostic assays described herein, and can also be included as components of kits (*e.g.*, reagent kits) for use in the screening and/or diagnostic assays described herein.

5 *Vectors*

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule of SEQ ID NOs: 1 or 3 or the complement thereof (or a portion thereof). Yet another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule encoding an amino acid of SEQ ID NO: 2 or polymorphic variant thereof. The constructs
10 comprise a vector (*e.g.*, an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a
15 "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-
20 episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, such as expression vectors, are capable of directing the expression of genes or nucleic acids to which they are
25 operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

30 Preferred recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the

nucleic acid molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, “operably linked” or “operatively linked” is intended to mean that the nucleic acid sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleic acid sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term “regulatory sequence” is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, “Gene Expression Technology”, *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleic acid sequence in many types of host cell and those which direct expression of the nucleic acid sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, *e.g.*, bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The

terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic acid molecule of the invention can be expressed in bacterial cells (*e.g.*, *E. coli*), insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene or nucleic acid that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene or nucleic acid of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector as the nucleic acid molecule of the invention or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be

identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene or nucleic acid will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic host cell or eukaryotic host cell in culture can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the invention has been introduced (*e.g.*, an exogenous FLAP nucleic acid, or an exogenous nucleic acid encoding a FLAP polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleic acid sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal include a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous

recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, *Current Opinion in BioTechnology* 2:823-829 (1991) and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.*, *Nature* 385:810-813 (1997) and PCT Publication Nos. WO 97/07668 and WO 97/07669.

POLYPEPTIDES OF THE INVENTION

The present invention also pertains to isolated polypeptides encoded by FLAP nucleic acids ("FLAP polypeptides"), and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (*e.g.*, other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell (*e.g.*, in a "fusion protein") and still be "isolated" or "purified."

The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of
5 considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes preparations of the polypeptide having less than about 30% (by dry weight) other proteins (*i.e.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less
10 than about 5% other proteins.

When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical
15 precursors or other chemicals" includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors
20 or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleic acid
25 sequence selected from the group consisting of SEQ ID NO: 1 or 3, or the complement of SEQ ID NO: 1 or 3, or portions thereof, or a portion or polymorphic variant thereof. However, the polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism,
30 *i.e.*, an allelic variant, as well as other splicing variants. Variants also encompass polypeptides derived from other genetic loci in an organism, but

having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1 or 3 or their complement, or portions thereof, or having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of nucleotide sequences encoding SEQ ID NO: 2 or polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, in certain embodiments at least about 70-75%, and in other embodiments at least about 80-85%, and in others greater than about 90% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to SEQ ID NO: 1 or 3 or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding SEQ ID NO: 2 or a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by a polypeptide encoded by a nucleic acid molecule of the invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as

conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.*, *Science* 255:306-312 (1992)).

The invention also includes fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising SEQ ID NO: 1 or 3, or the complement of SEQ ID NO: 1 or 3 (or other variants). However, the invention also encompasses
5 fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

10 Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, e.g., signal peptides, extracellular domains, one or more transmembrane segments or
15 loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one
20 embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These
25 comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide. "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect
30 function of the polypeptide *per se*. For example, the fusion polypeptide can be

5 a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of a polypeptide can be increased using a heterologous signal sequence. Therefore, in another embodiment, the fusion polypeptide contains a heterologous signal sequence at its N-terminus.

10 EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug discovery, for example, human proteins have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists. Bennett *et al.*, *Journal of Molecular Recognition*, 8:52-58 (1995) and Johanson *et al.*, *The Journal of Biological Chemistry*, 270,16:9459-9471 (1995). Thus, this invention also encompasses soluble fusion polypeptides containing a polypeptide of the invention and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE).

20 A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992).

Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

5 The isolated polypeptide can be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. In one embodiment, the polypeptide is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into
10 an expression vector, the expression vector introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

 The polypeptides of the present invention can be used to raise
15 antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the corresponding polypeptide is preferentially expressed,
20 either constitutively, during tissue differentiation, or in diseased states. The polypeptides can be used to isolate a corresponding binding agent, *e.g.*, ligand, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction. For
25 example, because members of the leukotriene pathway including FLAP bind to receptors, the leukotriene pathway polypeptides can be used to isolate such receptors.

ANTIBODIES OF THE INVENTION

 Polyclonal and/or monoclonal antibodies that specifically bind one
30 form of the polypeptide or nucleic acid product (*e.g.*, a polypeptide encoded by a nucleic acid having a SNP as set forth in Table 3), but not to another form

of the polypeptide or nucleic acid product, are also provided. Antibodies are also provided which bind a portion of either polypeptide encoded by nucleic acids of the invention (*e.g.*, SEQ ID NO: 1 or SEQ ID NO:3, or the complement of SEQ ID NO: 1 or SEQ ID NO:3), or to a polypeptide encoded by nucleic acids of the invention that contain a polymorphic site or sites. The invention also provides antibodies to the polypeptides and polypeptide fragments of the invention, or a portion thereof, or having an amino acid sequence encoded by a nucleic acid molecule comprising all or a portion of SEQ ID NOs: 1 or 3, or the complement thereof, or another variant or portion thereof.

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme

linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, *Nature* 256:495-497 (1975), the human B cell hybridoma technique (Kozbor *et al.*, *Immunol. Today* 4:72 (1983)); the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, 1985, Inc., pp. 77-96); or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.* (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, *e.g.*, *Current Protocols in Immunology*, *supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library

(e.g., an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP™* Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9: 1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246:1275-1281 (1989); Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (e.g., a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a polypeptide of the invention can be used to detect the polypeptide (e.g., in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by

coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

As described above, antibodies to leukotrienes can be used in the methods of the invention. The methods described herein can be used to generate such antibodies for use in the methods.

DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of MI or diagnosis of a susceptibility to MI or to a disease or condition associated with an MI gene, such as FLAP, as well as in kits useful for diagnosis of MI or a susceptibility to MI or to a disease or condition associated with FLAP. In one embodiment, the kit useful for diagnosis of MI or susceptibility to MI, or to a disease or condition associated with FLAP comprises primers as described herein, wherein the primers contain one or more of the SNPs identified in Table 3.

In one embodiment of the invention, diagnosis of MI or susceptibility to MI (or diagnosis of or susceptibility to a disease or condition associated with FLAP), is made by detecting a polymorphism in a FLAP nucleic acid as described herein. The polymorphism can be an alteration in a FLAP nucleic acid, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift alteration; the change of at least one

nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of the gene or nucleic acid; duplication of all or a part of the gene or nucleic acid; transposition of all or a part of the gene or nucleic acid; or rearrangement of all or a part of the gene or nucleic acid. More than one such alteration may be present in a single gene or nucleic acid. Such sequence changes cause an alteration in the polypeptide encoded by a FLAP nucleic acid. For example, if the alteration is a frame shift alteration, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a disease or condition associated with a FLAP nucleic acid or a susceptibility to a disease or condition associated with a FLAP nucleic acid can be a synonymous alteration in one or more nucleotides (*i.e.*, an alteration that does not result in a change in the polypeptide encoded by a FLAP nucleic acid). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the nucleic acid. A FLAP nucleic acid that has any of the alteration described above is referred to herein as an "altered nucleic acid."

In a first method of diagnosing MI or a susceptibility to MI, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, including all supplements through 1999). For example, a biological sample from a test subject (a "test sample") of genomic DNA, RNA, or cDNA, is obtained from an individual suspected of having, being susceptible to or predisposed for, or carrying a defect for, a susceptibility to a disease or condition associated with a FLAP nucleic acid (the "test individual"). The individual can be an adult, child, or fetus. The test

sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in an MI nucleic acid is present, and/or to determine which splicing variant(s) encoded by the FLAP is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the nucleic acid in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A "nucleic acid probe," as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain at least one polymorphism in a FLAP nucleic acid or contains a nucleic acid encoding a particular splicing variant of a FLAP nucleic acid. The probe can be any of the nucleic acid molecules described above (e.g., the nucleic acid, a fragment, a vector comprising the nucleic acid, a probe or primer, etc.).

To diagnose MI or a susceptibility to MI (or a disease or condition associated with FLAP), the test sample containing a FLAP nucleic acid is contacted with at least one nucleic acid probe to form a hybridization sample. A preferred probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs: 1 and 3, or the complement thereof or a portion thereof; or can be a nucleic acid encoding all or a portion of one of SEQ ID NO: 2. Other suitable probes for use in the diagnostic assays of the invention are described above (see e.g., probes and primers discussed under the heading, "Nucleic Acids of the Invention").

The hybridization sample is maintained under conditions that are sufficient to allow specific hybridization of the nucleic acid probe to a FLAP nucleic acid. "Specific hybridization," as used herein, indicates exact hybridization (*e.g.*, with no mismatches). Specific hybridization can be performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and FLAP nucleic acid in the test sample, then the FLAP has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the FLAP nucleic acid, or of the presence of a particular splicing variant encoding the FLAP nucleic acid, and is therefore diagnostic for a disease or condition associated with FLAP or a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI).

In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) the hybridization methods described above are used to identify the presence of a polymorphism or a particular splicing variant, associated with a disease or condition associated with or a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI). For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid probe, as described above, to RNA from the individual is indicative of a polymorphism in a FLAP nucleic acid, or of the presence of a particular splicing variant encoded by a FLAP nucleic acid, and is therefore diagnostic for the disease or condition associated with FLAP, or for susceptibility to a disease or condition associated with FLAP (*e.g.*, MI).

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents No. 5,288,611 and 4,851,330.

Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al.*, *Bioconjugate Chemistry* 5, American Chemical Society, p. 1 (1994)). The PNA probe can be designed to specifically hybridize to a nucleic acid having a polymorphism associated with a disease or condition associated with FLAP or associated with a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI). Hybridization of the PNA probe to a FLAP nucleic acid as described herein is diagnostic for the disease or condition or the susceptibility to the disease or condition.

In another method of the invention, mutation analysis by restriction digestion can be used to detect an altered nucleic acid, or nucleic acids containing a polymorphism(s), if the mutation or polymorphism in the nucleic acid results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a FLAP nucleic acid (and, if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology*, *supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the alteration or polymorphism in the FLAP nucleic acid, and therefore indicates the presence or absence of a disease or condition associated with FLAP or the susceptibility to a disease or condition associated with FLAP (*e.g.*, MI).

Sequence analysis can also be used to detect specific polymorphisms in the FLAP nucleic acid. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the nucleic acid, and/or its flanking sequences, if desired. The sequence of a

FLAP nucleic acid, or a fragment of the nucleic acid, or cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA, is determined, using standard methods. The sequence of the nucleic acid, nucleic acid fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known nucleic acid sequence of the nucleic acid, cDNA (*e.g.*, one or more of SEQ ID NOs: 1 or 3, and/or the complement of SEQ ID NO: 1 or 3), or a nucleic acid sequence encoding SEQ ID NO: 2 or a fragment thereof) or mRNA, as appropriate. The presence of a polymorphism in the FLAP indicates that the individual has disease or a susceptibility to a disease associated with FLAP (*e.g.*, MI).

Allele-specific oligonucleotides can also be used to detect the presence of polymorphism(s) in the FLAP nucleic acid, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, for example, approximately 15-30 base pairs, that specifically hybridizes to a FLAP nucleic acid, and that contains a polymorphism associated with a disease or condition associated with FLAP or a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI). An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a FLAP nucleic acid can be prepared, using standard methods (see *Current Protocols in Molecular Biology, supra*). To identify polymorphisms in the nucleic acid associated with disease or susceptibility to disease, a test sample of DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a FLAP nucleic acid, and its flanking sequences. The DNA containing the amplified FLAP nucleic acid (or fragment of the nucleic acid) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology, supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe

to the amplified FLAP is then detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the FLAP, and is therefore indicative of a disease or condition associated with FLAP or a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI).

An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (*see, e.g.*, WO 93/22456).

With the addition of such analogs as locked nucleic acids (LNAs), the size of primers and probes can be reduced to as few as 8 bases. LNAs are a novel class of bicyclic DNA analogs in which the 2' and 4' positions in the furanose ring are joined via an O-methylene (oxy-LNA), S-methylene (thio-LNA), or amino methylene (amino-LNA) moiety. Common to all of these LNA variants is an affinity toward complementary nucleic acids, which is by far the highest reported for a DNA analog. For example, particular all oxy-LNA nonamers have been shown to have melting temperatures of 64°C and 74°C when in complex with complementary DNA or RNA, respectively, as opposed to 28°C for both DNA and RNA for the corresponding DNA nonamer. Substantial increases in T_m are also obtained when LNA monomers are used in combination with standard DNA or RNA monomers. For primers and probes,

depending on where the LNA monomers are included (*e.g.*, the 3' end, the 5' end, or in the middle), the T_m could be increased considerably.

5 In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a FLAP nucleic acid. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also described as "Genechips™," have been generally described in the art, for example, U.S. Pat. No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and WO 92/10092. These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods that incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See Fodor *et al.*, 10 *Science* 251:767-777 (1991); Pirrung *et al.*, U.S. Pat. 5,143,854; (see also PCT Application WO 90/15070); Fodor *et al.*, PCT Publication WO 92/10092; and U.S. Pat. 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Pat. 5,384,261, the entire teachings of which are incorporated by reference herein. In another 20 example, linear arrays can be utilized.

Once an oligonucleotide array is prepared, a nucleic acid of interest is hybridized with the array and scanned for polymorphisms. Hybridization and scanning are generally carried out by methods described herein and also in, 25 *e.g.*, published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. No. 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence that includes one or more previously identified polymorphic markers is amplified using well-known amplification techniques, *e.g.*, PCR. Typically, this involves the use of 30 primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism.

Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array. In a reverse method, a probe, containing a polymorphism, can be coupled to a solid surface and PCR amplicons are then added to hybridize to these probes.

Although primarily described in terms of a single detection block, *e.g.*, detection of a single polymorphism arrays can include multiple detection blocks, and thus be capable of analyzing multiple, specific polymorphisms. It will generally be understood that detection blocks may be grouped within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional uses of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patents Nos. 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein. Other methods of nucleic acid analysis can be used to detect polymorphisms in a nucleic acid described herein, or variants encoded by a nucleic acid described herein. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al.*, *Proc. Natl. Acad. Sci., USA* 74:5463-5467 (1977); Beavis *et al.* U.S. Pat. No. 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)),

mobility shift analysis (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

In one embodiment of the invention, diagnosis of a disease or condition associated with FLAP (*e.g.*, MI) or a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI) can also be made by expression analysis by quantitative PCR (kinetic thermal cycling). This technique utilizing TaqMan[®] can be used to allow the identification of polymorphisms and whether a patient is homozygous or heterozygous. The technique can assess the presence of an alteration in the expression or composition of the polypeptide encoded by a FLAP nucleic acid or splicing variants encoded by a FLAP nucleic acid. Further, the expression of the variants can be quantified as physically or functionally different.

In another embodiment of the invention, diagnosis of MI or a susceptibility to MI (or of another disease or condition associated with FLAP) can also be made by examining expression and/or composition of a FLAP polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a FLAP nucleic acid, or for the presence of a particular variant encoded by a FLAP nucleic acid. An alteration in expression of a polypeptide encoded by a FLAP nucleic acid can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by a FLAP nucleic acid is an alteration in the qualitative polypeptide expression (*e.g.*, expression of an altered FLAP polypeptide or of

a different splicing variant). In a preferred embodiment, diagnosis of disease or condition associated with FLAP or a susceptibility to a disease or condition associated with FLAP is made by detecting a particular splicing variant encoded by that FLAP variant, or a particular pattern of splicing variants.

5 Both such alterations (quantitative and qualitative) can also be present. An "alteration" in the polypeptide expression or composition, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by a FLAP nucleic acid in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*,
10 is from the same type of cells), and is from an individual who is not affected by the disease or a susceptibility to a disease or condition associated with a FLAP nucleic acid. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of disease or condition associated with FLAP or a susceptibility to a
15 disease or condition associated with FLAP (*e.g.*, MI). Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated with a FLAP nucleic acid. Various means of
20 examining expression or composition of the polypeptide encoded by a FLAP nucleic acid can be used, including: spectroscopy, colorimetry, electrophoresis, isoelectric focusing and immunoassays (*e.g.*, David *et al.*, U.S. Pat. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one
25 embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass
30 direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of

the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by an altered FLAP (*e.g.*, by a FLAP having a SNP as shown in Table 3), or an antibody that specifically binds to a polypeptide encoded by a non-altered nucleic acid, or an antibody that specifically binds to a particular splicing variant encoded by a nucleic acid, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or altered FLAP, or the absence in a test sample of a particular splicing variant or of a polypeptide encoded by a non-polymorphic or non-altered nucleic acid. The presence of a polypeptide encoded by a polymorphic or altered nucleic acid, or the absence of a polypeptide encoded by a non-polymorphic or non-altered nucleic acid, is diagnostic for disease or condition associated with FLAP or a susceptibility to a disease or condition associated with, as is the presence (or absence) of particular splicing variants encoded by the FLAP nucleic acid.

In one embodiment of this method, the level or amount of polypeptide encoded by a FLAP nucleic acid in a test sample is compared with the level or amount of the polypeptide encoded by the FLAP in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the FLAP, and is diagnostic for disease or condition, or for a susceptibility to a disease or condition, associated with that FLAP. Alternatively, the composition of the polypeptide encoded by a FLAP nucleic acid in a test sample is compared with the composition of the polypeptide encoded by the FLAP in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide

in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a disease or condition, or for a susceptibility to a disease or condition, associated with that FLAP. In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a disease or condition, or a susceptibility to a disease or condition, associated with FLAP (*e.g.*, MI).

The invention further pertains to a method for the diagnosis and identification of susceptibility to myocardial infarction in an individual, by identifying an at-risk haplotype in FLAP. In one embodiment, the at-risk haplotype is one which confers a significant risk of MI. In one embodiment, significance associated with a haplotype is measured by an odds ratio. In a further embodiment, the significance is measured by a percentage. In one embodiment, a significant risk is measured as an odds ratio of at least about 1.2, including by not limited to: 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, and 1.9. In a further embodiment, an odds ratio of at least 1.2 is significant. In a further embodiment, an odds ratio of at least about 1.5 is significant. In a further embodiment, a significant increase in risk is at least about 1.7 is significant. In a further embodiment, a significant increase in risk is at least about 20%, including but not limited to about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95, and 98%. In a further embodiment, a significant increase in risk is at least about 50%. It is understood however, that identifying whether a risk is medically significant may also depend on a variety of factors, including the specific disease, the haplotype, and often, environmental factors.

The invention also pertains to methods of diagnosing a susceptibility to myocardial infarction in an individual, comprising screening for an at-risk haplotype in the FLAP nucleic acid that is more frequently present in an

individual susceptible to myocardial infarction (affected), compared to the frequency of its presence in a healthy individual (control), wherein the presence of the haplotype is indicative of susceptibility to myocardial infarction. Standard techniques for genotyping for the presence of SNPs and/or microsatellite markers that are associated with myocardial infarction can be used, such as fluorescent based techniques (Chen, *et al.*, *Genome Res.* 9, 492 (1999), PCR, LCR, Nested PCR and other techniques for nucleic acid amplification. In a preferred embodiment, the method comprises assessing in an individual the presence or frequency of SNPs and/or microsatellites in the FLAP nucleic acid that are associated with myocardial infarction, wherein an excess or higher frequency of the SNPs and/or microsatellites compared to a healthy control individual is indicative that the individual is susceptible to myocardial infarction.

See table 9 for SNPs that comprise haplotypes that can be used as screening tools. See also Table 3 that sets forth SNPs and markers for use as screening tools.

In one embodiment, the at-risk haplotype is characterized by the presence of polymorphism(s) represented in Table 3. For example, DG00AAFIU at position 256047, where the SNP can be a "C" or a "T"; SG13S25 at position 283477, where the SNP can be a "G" or an "A"; DG00AAJFF at position 287889, where the SNP can be a "G" or an "A"; DG00AAHII at position 294503, where the SNP can be a "G" or an "A"; DG00AAHID at position 296020, where the SNP can be a "T" or an "A"; B_SNP_310657 at position 310657, where the SNP can be a "G" or an "A"; SG13S30 at position 312056, where the SNP can be a "G" or a "T"; SG13S32 at position 316763, where the SNP can be a "C" or an "A"; SG13S42 at position 320393, where the SNP can be a "G" or an "A"; and SG13S35 at position 324333, where the SNP can be a "G" or an "A".

Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as described herein (*e.g.*, labeled

probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP analysis), allele-specific oligonucleotides, antibodies which bind to altered or to non-altered (native) FLAP polypeptide, means for amplification of nucleic acids comprising a FLAP, or means for analyzing the nucleic acid sequence of a nucleic acid described herein, or for analyzing the amino acid sequence of a polypeptide as described herein, etc. In one embodiment, a kit for diagnosing MI or susceptibility to MI can comprise primers for nucleic acid amplification of a region in the FLAP nucleic acid comprising an at-risk haplotype that is more frequently present in an individual having MI or susceptible to MI. The primers can be designed using portions of the nucleic acids flanking SNPs that are indicative of MI. In a particularly preferred embodiment, the primers are designed to amplify regions of the FLAP nucleic acid associated with an at-risk haplotype for MI, as shown in Table 9, or more particularly the haplotype defined by the following SNP markers: In one embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers DG00AAFIU, SG13S25, DG00AAJFF, DG00AAHII, SG13S32 and SG13S35 at the 13q12 locus. In one particular embodiment, the presence of the alleles T, G, G, G, A and G at DG00AAFIU, SG13S25, DG00AAJFF, DG00AAHII, SG13S32 and SG13S35, respectively (the B6 haplotype), is diagnostic of susceptibility to myocardial infarction. In another embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers DG00AAFIU, SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In one particular embodiment, the presence of the alleles T, G, G, G and A at DG00AAFIU, SG13S25, DG00AAHII, SG13S30 and SG13S42, respectively (the B5 haplotype), is diagnostic of susceptibility to myocardial infarction. In a third embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In one particular embodiment, the presence of the alleles G, G, G and A at SG13S25, DG00AAHII, SG13S30 and SG13S42, respectively (the B4 haplotype), is diagnostic of susceptibility to myocardial

infarction. In a fourth embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers DG00AAFTU, SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus. In one particular embodiment, the presence of the alleles T, G, T, G and A at DG00AAFTU, SG13S25, DG00AAHID, B_SNP_310657 and SG13S32, respectively (the A5 haplotype), is diagnostic of susceptibility to myocardial infarction. In a fifth embodiment, a haplotype associated with a susceptibility to myocardial infarction comprises markers SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus. In one particular embodiment, the presence of the alleles G, T, G and A at SG13S25, DG00AAHID, B_SNP_310657 and SG13S32, respectively (the A4 haplotype), is diagnostic of susceptibility to myocardial infarction.

SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

The invention provides methods (also referred to herein as “screening assays”) for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs: 1 or 3 or the complement thereof, or a nucleic acid encoding an amino acid having the sequence of SEQ ID NO: 2, or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In a preferred embodiment, high stringency conditions are conditions appropriate for selective hybridization. In another embodiment, a sample containing a nucleic acid molecule of interest is contacted with a nucleic acid containing a contiguous nucleic acid sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of

the nucleic acid molecule of interest (*e.g.*, a FLAP nucleic acid), and the contacted sample is assessed for the presence or absence of hybridization. In a preferred embodiment, the nucleic acid containing a contiguous nucleic acid sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be subjected to amplification prior to performing the hybridization.

In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described above), and then assessing the sample for the presence (or absence) of binding of the antibody to the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes which alter (*e.g.*, increase or decrease) the activity of the polypeptides described herein, or which otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, binding agent for members of the leukotriene pathway, such as FLAP binding agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with members of the leukotriene pathway binding agents (*e.g.*, receptors or other binding agents); or which alter posttranslational processing of the leukotriene pathway member polypeptide, such as a FLAP polypeptide (*e.g.*, agents that alter proteolytic processing to direct the polypeptide from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.)

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays. Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the “one-bead one-compound” library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a FLAP polypeptide, a cell, cell lysate, or solution containing or expressing a FLAP polypeptide (*e.g.*, SEQ ID NO: 2 or another splicing variant encoded by a FLAP nucleic acid, such as a nucleic acid comprising a SNP as shown in Table 3), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of FLAP activity is assessed (*e.g.*, the level (amount) of FLAP activity is measured, either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity of the FLAP polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of a FLAP polypeptide. An increase in the level of FLAP activity in the presence of the agent relative to the activity in the absence of the agent, indicates that the agent is an agent that enhances (is an agonist of) FLAP activity. Similarly, a decrease in the level of FLAP activity in the presence of the agent, relative to the activity in the absence of the agent, indicates that the agent is an agent that inhibits (is an

antagonist of) FLAP activity. In another embodiment, the level of activity of a FLAP polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A statistically significant difference in the level of the activity in the presence of the agent from the control level indicates that the agent alters FLAP activity.

The present invention also relates to an assay for identifying agents which alter the expression of a FLAP nucleic acid (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes; which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the nucleic acid or which otherwise interact with the nucleic acids described herein, as well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a FLAP polypeptide (*e.g.*, a FLAP nucleic acid) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution can be another solution that comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of FLAP expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level and/or pattern of expression in a control (*i.e.*, the level and/or pattern of the FLAP expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differ, by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of the FLAP nucleic acid. Enhancement of FLAP expression indicates that the agent is an agonist of FLAP activity. Similarly, inhibition of FLAP expression indicates that the agent is an antagonist of FLAP activity.

In another embodiment, the level and/or pattern of FLAP polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that have previously been established. A level and/or pattern in the presence of the agent that
5 differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters FLAP expression.

In another embodiment of the invention, agents which alter the expression of a FLAP nucleic acid or which otherwise interact with the nucleic acids described herein, can be identified using a cell, cell lysate, or solution
10 containing a nucleic acid encoding the promoter region of the FLAP nucleic acid operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*, the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter gene in the absence
15 of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression of the FLAP nucleic acid, as indicated by its ability to alter expression of a nucleic acid that is operably linked to the FLAP nucleic acid promoter.

Enhancement of the expression of the reporter indicates that the agent
20 is an agonist of FLAP activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of FLAP activity. In another embodiment, the level of expression of the reporter in the presence of the test agent, is compared with a control level that has previously been established.
25 A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters expression.

Agents which alter the amounts of different splicing variants encoded by a FLAP nucleic acid (*e.g.*, an agent which enhances activity of a first
30 splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and

antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide relative to a FLAP binding agent. For example, a cell that expresses a compound that interacts with a FLAP nucleic acid (herein referred to as a "FLAP binding agent", which can be a polypeptide or other molecule that interacts with a FLAP nucleic acid, such as a receptor, or another molecule, such as 5-LO) is contacted with a FLAP in the presence of a test agent, and the ability of the test agent to alter the interaction between the FLAP and the FLAP binding agent is determined. Alternatively, a cell lysate or a solution containing the FLAP binding agent, can be used. An agent which binds to the FLAP or the FLAP binding agent can alter the interaction by interfering with, or enhancing the ability of the FLAP to bind to, associate with, or otherwise interact with the FLAP binding agent. Determining the ability of the test agent to bind to a FLAP nucleic acid or a FLAP nucleic acid binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with ^{125}I , ^{35}S , ^{14}C or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. It is also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent with a FLAP or a FLAP binding agent without the labeling of either the test agent, FLAP, or the FLAP binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a "microphysiometer" (e.g., CytosensorTM) is an analytical instrument that measures the rate at which a cell acidifies its environment

using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between ligand and polypeptide.

Thus, these receptors can be used to screen for compounds that are agonists for use in treating a disease or condition associated with FLAP or a susceptibility to a disease or condition associated with FLAP, or antagonists for studying a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI). Drugs can be designed to regulate FLAP activation, that in turn can be used to regulate signaling pathways and transcription events of genes downstream or of proteins or polypeptides interacting with FLAP (*e.g.*, 5-LO).

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more FLAP polypeptides, as described herein. For example, a yeast two-hybrid system such as that described by Fields and Song (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more FLAP polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor that has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (*e.g.*, nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a FLAP polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the FLAP polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a FLAP polypeptide binding agent or receptor). Incubation of yeast containing the first vector and the second vector under appropriate conditions (*e.g.*, mating conditions such as used in the

Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies that express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the FLAP polypeptide or fragment or derivative thereof. Such polypeptides may be useful as agents that alter the activity of expression of a FLAP polypeptide, as described above.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either the FLAP, the FLAP binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that allows a FLAP nucleic acid or a FLAP binding agent to be bound to a matrix or other solid support.

In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a nucleic acid encoding a FLAP nucleic acid is contacted with a test agent and the expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test agent is identified as a stimulator or enhancer of the mRNA or polypeptide

expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by methods described herein for detecting mRNA or polypeptide.

In yet another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) the activity of a member of leukotriene pathway binding agent, such as a FLAP binding agent (*e.g.*, 5-LO), as described herein. For example, such agents can be agents which have a stimulatory or inhibitory effect on, for example, the activity of a member of leukotriene pathway binding agent, such as a FLAP binding agent; which change (*e.g.*, enhance or inhibit) the ability a member of leukotriene pathway binding agents, (*e.g.*, receptors or other binding agents) to interact with the polypeptides of the invention; or which alter posttranslational processing of the member of leukotriene pathway binding agent, (*e.g.*, agents that alter proteolytic processing to direct the member of the leukotriene pathway binding agent from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more active binding agent is released from the cell, etc.).

For example, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of a member of the leukotriene pathway (or enzymatically active portion(s) thereof), as well as agents identifiable by the assays. As described above, test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological

library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S. *Anticancer Drug Des.*, 12:145 (1997)).

5 In one embodiment, to identify agents which alter the activity of a member of the leukotriene pathway (such as a FLAP binding agent, or an agent which binds to a member of the leukotriene pathway (a "binding agent")), a cell, cell lysate, or solution containing or expressing a binding agent (*e.g.*, 5-LO, or a leukotriene pathway member receptor, or other binding agent), or a fragment (*e.g.*, an enzymatically active fragment) or derivative thereof, can be contacted with an agent to be tested; alternatively, the binding agent (or fragment or derivative thereof) can be contacted directly with the agent to be tested. The level (amount) of binding agent activity is assessed (either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of the member of the leukotriene pathway. An increase in the level of the activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) the activity. Similarly, a decrease in the level of activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) the activity. In another embodiment, the level of activity in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters the activity.

 This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described

herein (*e.g.*, a test agent that is a modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described
5 herein can be used in an animal model to determine the mechanism of action of such an agent.

Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an agent identified as described herein can be used to alter activity of
10 a polypeptide encoded by a FLAP nucleic acid, or to alter expression of a FLAP nucleic acid, by contacting the polypeptide or the nucleic acid (or contacting a cell comprising the polypeptide or the nucleic acid) with the agent identified as described herein.

15 The present invention is now illustrated by the following Examples, which are not intended to be limiting in any way. The teachings of all references cited are incorporated herein in their entirety.

20 EXAMPLE 1: IDENTIFICATION OF GENE AND HAPLOTYPES ASSOCIATED WITH MI

SUBJECTS AND METHODS

Study population

25 Patients entering the study were defined from an infarction registry that includes all MIs (over 8,000 patients) in Iceland 1981-2000. This registry is a part of the World Health Organization MONICA Project (The World Health Organization MONICA Project (monitoring trends and determinants in cardiovascular disease): a major international collaboration. (WHO MONICA Project Principal Investigators. *J Clin. Epidemiol.* 1988; 41:105-14). Diagnosis of all patients in the registry follow strict

diagnostic rules based on symptoms, electrocardiograms, cardiac enzymes, and necropsy findings.

Blood samples from 570 female MI patients and 1380 male patients, both cases with a family history and sporadic cases were collected. For each patient that participated, blood was collected from 2 relatives (unaffected or affected). Their genotypes were used to help with construction of haplotypes.

Linkage analysis

One hundred and sixty female MI patients were clustered into large extended families such that each patient is related to at least one other patient within and including six meiotic events (*e.g.*, 6 meiotic events separate second cousins). The information regarding the relatedness of patients was obtained from an encrypted genealogy database that covers the entire Icelandic nation (Gulcher *et al.*, *Eur. J. Hum. Genet.* 8: 739-742 (2000)). A genomewide scan was performed using a framework map of 1000 microsatellite markers, using protocols described elsewhere (Gretarsdottir S., *et al. Am. J. Hum. Genet.*, 70: 593-603, 2002)). The marker order and positions were obtained from deCODE genetics' high resolution genetic map (Kong A, *et al.*, *Nat. genet.*, 31: 241-247 (2002)). The population-based allelic frequencies were constructed from a cohort of more than 30,000 Icelanders who have participated in genetic studies of various disease projects. Additional markers were genotyped within the highest linkage peak on chromosome 13 to increase the information on identity by descent within the families. For those markers at least 180 Icelandic controls were genotyped to derive the population allele frequencies.

For statistical analysis, multipoint, affected-only allele-sharing methods were used to assess evidence for linkage. All results, both the LOD and the non-parametric linkage (NPL) score, were obtained using the program ALLEGRO (Gudbjartsson D.F., *et al.*, *Nat Genet.*, 25: 12-13(2000)). The baseline linkage analysis (Gretarsdottir S., *et al.*, *Am. J. Hum. Genet.* 70: 593-603, (2002)) uses the Spairs scoring function (Whittermore AS, and Haplern J

A., *Biometrics* 50: 118-127 (1994)) and Kruglyak *et al.*, *Am. J. Hum. Genet.*, 58:1347-1363 (1996)) the exponential allele-sharing model (Kong A., and Cox N.J., *Am. J. Hum. Genet.* 61:1179-1188 (1997)), and a family weighting scheme which is halfway, on the log-scale, between weighing each affected pairs equally and weighing each family equally.

Ultra-fine mapping and haplotype analysis:

A candidate susceptibility locus was defined as the region under the LOD score curve where the score was one lod lower than the highest lod score. This region (approx. 12Mb) was ultra-finemapped with microsatellite markers with an average spacing between markers of less than 100Kb. All usable microsatellite markers found in public databases and mapped within that region were used. In addition, microsatellite markers identified within the deCODE genetics sequence assembly of the human genome were used.

Haplotype analysis.

The frequencies of haplotypes were estimated in the patient and the control groups using an expectation-maximization algorithm (Dempster A.P. *et al.*, *J. R. Stat. Soc. B.* 39: 1-389 (1977)). An implementation of this algorithm that can handle missing genotypes and uncertainty with the phase was used. Under the null hypothesis, the patients and the controls are assumed to have identical frequencies. Using a likelihood approach, an alternative hypothesis where a candidate at-risk-haplotype is allowed to have a higher frequency in patients than controls, while the ratios of the frequencies of other haplotypes are assumed to be the same in both groups was tested. Likelihoods are maximized separately under both hypothesis and a corresponding 1-df likelihood ratio statistics is used to evaluate the statistic significance.

To look for at-risk-haplotypes in the 1-lod drop, association of all possible combinations of genotyped markers was studied, provided those markers spanned a region of size less than 1000 Kb. Due to a certain amount of testing, the *p*-values were adjusted using simulations. The combined

patient and control groups were randomly divided into two sets, equal in size to the original group of patients and controls. The haplotype analysis was then repeated and the most significant p -value registered was observed. This randomization scheme was repeated over 100 times to construct an empirical distribution of p -values.

Results and Discussion

In a genome wide search for susceptibility genes for MI, a locus was mapped to a location on chromosome 13q12. FIG. 1 shows the multipoint non-parametric LOD scores a linkage scan for a framework marker map on chromosome 13. A LOD score suggestive of linkage of 2.5 was found centered at marker D13S289. The marker map for chromosome 13 that was used in the linkage analysis is shown in Table 1. The LOD score at this location remained with increased number of microsatellite markers which increased information content of the linkage (FIG. 2).

A very large number of microsatellite markers were then added within the central 12 megabase (Mb) segment under the LOD score defined by the drop in one LOD from the peak marker. FIG. 3A shows the results from a haplotype association case-control analysis of 437 female MI patients versus 721 controls using combinations of 4 and 5 microsatellite markers to define the test haplotypes. The most significant microsatellite marker haplotype association across this entire 12 Mb segment was found using markers DG13S1103, DG13S166, DG13S1287, DG13S1061 and DG13S301, with alleles 4, 0, 2, 14 and 3, respectively (p -value of 1.02×10^{-7}). Carrier frequency of this haplotype is 7.3% in female MI patients and 0.3% in controls. There are several other haplotypes that show great association to MI that overlap the first haplotype. The 80Kb segment that is defined by two markers (DG13S166 and D13S1238) common to all the haplotypes shown in the figure includes only one gene, FLAP (ALOX5AP). A two marker haplotype involving alleles 0 and -2 for markers DG13S166 and D13S1238, respectively, is found in excess in patients. Carrier frequency of this

-117-

haplotype was estimated to be 27% in female MI patients and 15.4% in controls (p -value 1×10^{-3}). This was our first evidence that variation in the FLAP gene contributes to MI risk.

To confirm this observation, the FLAP gene was sequenced in its entirety and numerous SNPs were defined. Many of these were used to genotype 437 female MI patients, 1049 male MI patients, and 811 controls. In a case-control study of the MI patients using these data, several haplotypes were found, that were significantly over-represented in the female MI patients compared to controls (see Table 6). These haplotypes were highly correlated to each other since they are within a block of linkage disequilibrium covering the FLAP gene. Table 7 shows two haplotypes that are representative of these female MI risk haplotypes. They have relative risks of 2.4 and 4 and are carried by 23% and 13% of female MI patients, respectively. Table 8 shows that these same haplotypes show association to male MI although with lower relative risks.

In an effort to identify haplotypes involving only SNP markers that associate with MI, more SNPs were identified by sequencing the FLAP gene and the region flanking the gene. Currently, a total number of 45 SNPs have been genotyped on 1343 patients and 624 unrelated controls. Two correlated series of SNP haplotypes were observed in excess in patients, denoted as A and B in Table 9. The length of the haplotypes varies between 33 and 69 Kb, and the haplotypes cover one or two blocks of linkage disequilibrium. Both series of haplotypes contain the common allele 2 of the SNP SG13S25. All haplotypes in the A series contain the SNP DG00AAHID, while all haplotypes in the B series contain the SNP DG00AAHII. In the B series, the haplotypes B4, B5, and B6 have a relative risk (RR) greater than 2 and with allelic frequencies above 10%. The haplotypes in A series have slightly lower RR and lower p -values, but higher frequency (15-16%). The haplotypes in series B and A are strongly correlated, i.e. the haplotypes in B define a subset of the haplotypes in A. Hence, haplotypes B are more specific than A. Haplotypes A are however more sensitive, i.e. they capture more individuals with the

putative mutation, as is observed in the population attributable risk which is less for B than for A. Furthermore, these haplotypes show similar risk ratios and allelic frequency for early-onset patients (defined as onset of first MI before the age of 55) and for both gender. In addition, analyzing various groups of patients with known risk factors, such as hypertension, high cholesterol, smoking and diabetes, did not reveal any significant correlation with these haplotypes, indicating that the haplotypes in the FLAP gene represent an independent genetic susceptibility factor for MI.

The FLAP gene encodes for a protein that is required for leukotriene synthesis (LTA₄, LTB₄, LTC₄, LTD₄, LTE₄). Inhibitors of its function impede translocation of 5-lipoxygenase from the cytoplasm to the cell membrane and inhibit activation of 5-lipoxygenase. The leukotrienes are potent inflammatory lipid mediators derived from arachidonic acid that can potentially contribute to development of atherosclerosis and destabilization of atherosclerotic plaques through lipid oxidation and/or proinflammatory effects. Allen *et al.*, (*Circulation*. 97: 2406-2413(1998)) described a novel mechanism in which atherosclerosis is associated with the appearance of a leukotriene receptor(s) capable of inducing hyperreactivity of human epicardial coronary arteries in response to LTC₄ and LTD₄. Allen *et al.* show a photomicrograph of a section of human atherosclerotic coronary artery a positive staining of a number of members of the leukotriene pathway, including FLAP. Mehrabian *et al.* described the identification of 5-Lipoxygenase (5-LO) as a major gene contributing to atherosclerosis susceptibility in mice. Mehrabian *et al.* described that heterozygous deficiency for the enzyme in a knockout model decreased the atherosclerotic lesion size in LDL^{-/-} mice by about 95%. Mehrabian *et al.* show that the enzyme is expressed abundantly in macrophage-rich regions of atherosclerotic lesions, and suggested that 5-LO and/or its products might act locally to promote lesion development (Mehrabian *et al.*, *Circulation Research*. 91:120 (2002)). Studies of FLAP inhibition in animal models of atherosclerosis are scarce. However, in a rabbit model of acute MI assessed 72 hours after coronary artery ligation the FLAP-inhibitor

BAYx1005 *markedly* reduced mortality, from 65% to 25%, and blocked the increase in CPK and neutrophil accumulation as well as the ECG-changes observed in sham treated animals (*J. Pharmacol. Exp. Ther.*, 276:332 (1996)).

Mutations and /or polymorphisms within the FLAP nucleic acid, and other members of the same pathway (e.g., 5-lipoxygenase, LTA4 Hydrolase, LTB4 receptors, LTC4 Synthase, and CysLT2 receptor), that show association with the disease, can be used as a diagnostic test. The members of the 5-LO pathway in particular are valuable therapeutic targets for myocardial infarction.

Table 1 The marker map for chromosome 13 used in the linkage analysis.

Location (cM)	Marker	Location (cM)	Marker
6	D13S175	63.9	D13S170
9.8	D13S1243	68.7	D13S265
13.5	D13S1304	73	D13S167
17.2	D13S217	76.3	D13S1241
21.5	D13S289	79.5	D13S1298
25.1	D13S171	81.6	D13S1267
28.9	D13S219	84.7	D13S1256
32.9	D13S218	85.1	D13S158
38.3	D13S263	87	D13S274
42.8	D13S326	93.5	D13S173
45.6	D13S153	96.7	D13S778
49.4	D13S1320	102.7	D13S1315
52.6	D13S1296	110.6	D13S285
55.9	D13S156	115	D13S293
59.8	D13S1306		

Table 2 Marker Map for the second step of Linkage Analysis

Location (cM)	Marker	Location (cM)	Marker
1.758	D13S175	42.585	D13S1248
9.235	D13S787	44.288	D13S1233
11.565	D13S1243	44.377	D13S263
16.898	D13S221	45.535	D13S325
17.454	D13S1304	45.536	D13S1270
18.011	D13S1254	45.537	D13S1276
18.59	D13S625	49.149	D13S326
19.308	D13S1244	49.532	D13S1272
19.768	D13S243	52.421	D13S168
22.234	D13S1250	52.674	D13S287
22.642	D13S1242	60.536	D13S1320
22.879	D13S217	64.272	D13S1296
25.013	D13S1299	71.287	D13S156
28.136	D13S289	76.828	D13S1306
28.678	D13S290	77.86	D13S170
29.134	D13S1287	82.828	D13S265
30.073	D13S260	91.199	D13S1241
31.98	D13S171	93.863	D13S1298
32.859	D13S267	97.735	D13S779
33.069	D13S1293	100.547	D13S1256
33.07	D13S620	102.277	D13S274
34.131	D13S220	111.885	D13S173
36.427	D13S219	112.198	D13S796
39.458	D13S1808	115.619	D13S778
40.441	D13S218	119.036	D13S1315
41.113	D13S1288	126.898	D13S285
41.996	D13S1253	131.962	D13S293

-121-

Table 3 shows the five exons with positions that encode the FLAP protein, markers, polymorphisms and SNPs identified within the genomic sequence by the methods described herein. One SNP, B_SNP_302465, is in the coding region. The polymorphism, SNP 302465, does not change the amino acid sequence in the protein.

Table 3 Exons and SNPs in the Nucleic Acid Encoding FLAP

Exons/markers/SNPs	Position(bp)	Size(bp)	SNPs	
D13S289	249198-249445	248		
DG13S166	249855-250249	395		
Exon1	293667-293736	70		
Exon2	302413-302512	100		
B_SNP_302465	302465	1	heterozygous C-T (3%)	in exon
B_SNP_302524	302524	1	heterozygous A-C (55%)	
			homozygous A-A (22.5%)	
			homozygous C-C (22.5%)	
B_SNP_302560	302560	1	heterozygous A-G (2%)	
B_SNP_302617	302617	1	heterozygous C-T (37%)	
			homozygous T-T (59%)	
			homozygous C-C (4%)	
Exon3	310405-310475	71		
B_SNP_310657	310657	1	heterozygous A-G (6%)	
Exon4	314297-314378	82		
B_SNP_314500	314500	1	heterozygous G-C (24%)	
			homozygous C-C (6%)	
			Homozygous G-G (70%)	
Exon5	322297-322459	163		
DG13S164	330669-330886	218		
D13S1238	330679-330831	153		
DG13S163	363743-363904	162		
SNP13B_R1028729	145600	1	homozygous C-C (11%),	
(rs1028729)			heterozygous C-T (41%)	
			homozygous T-T (47%)	
SNP13B_Y1323898	151047	1	homozygous G-G (38%)	
(rs1323898)*			heterozygous G-A (47%)	
			homozygous A-A (15%)	

SNP13B K912392				
(rs912392)*	193119	1	homozygous C-C (13%)	
			heterozygous C-T (46%)	
			homozygous T-T (41%)	
DG00AAFQR				
(rs1556428)*	117676	1	homozygous G-G (1%)	
			heterozygous G-A (18%)	
			homozygous A-A (80%)	
DG00AAFIV				
(rs22485654)*	227629	1	homozygous T-T (75%)	
			heterozygous T-A (23%)	
			homozygous A-A (2%)	
DG00AFJT	293754	1	homozygous C-C (45%),	
			heterozygous C-A (45%),	
			homozygous A-A (10%)	
DG00AAHII	294503	1	homozygous G-G (44%),	
			heterozygous G-A (46%),	
			homozygous A-A (10%)	
DG00AAHID	296020	1	homozygous T-T (43%),	
			heterozygous T-A (45%),	
			homozygous A-A (12%)	
DG00AAHIJ	298098	1	homozygous G-G (60%),	
			heterozygous G-A (35%),	
			homozygous A-A (6%)	
DG00AAHIH	298188	1	homozygous G-G (32%),	
			heterozygous G-A (48%),	
			homozygous A-A (19%)	
DG00AAHIE				
(rs3885907)*	298379	1	homozygous C-C (23%),	
			heterozygous C-A (48%),	
			homozygous A-A (29%)	
DG00AAHIG	304334	1	homozygous C-C (21%),	
			heterozygous C-T (49%),	
			homozygous T-T (31%)	
DG00AAHIF	324849	1	homozygous G-G (54%),	
			heterozygous G-C (39%),	
			homozygous C-C (7%)	

-123-

DG00AAHOI	325651	1	homozygous G-G (59%),
			heterozygous G-A (36%),
			homozygous A-A (5%)
FLA267479	267479	1	
FLA267696	267696	1	
FLA267853	267853	1	
FLA270742	270742	1	
FLA270830	270830	1	
FLA273407	273407	1	
FLA274084	274084	1	
FLA275784	275784	1	
FLA275952	275952	1	
FLA277478	277478	1	
FLA277678	277678	1	
FLA278185	278185	1	
FLA278492	278492	1	
FLA278845	278845	1	
FLA280183	280183	1	
FLA280923	280923	1	
FLA283400	283400	1	
FLA283477/SG13S25	283477	1	
FLA284410	284410	1	
FLA284815	284815	1	
FLA284903	284903	1	
FLA290195	290195	1	
FLA290553	290553	1	
FLA290570	290570	1	
FLA292253	292253	1	
FLA292576	292576	1	
FLA295036	295036	1	
FLA296102	296102	1	
FLA298098	298098	1	
FLA298188	298188	1	
FLA298230	298230	1	
FLA298379	298379	1	
FLA298507	298507	1	
FLA298604	298604	1	
FLA298987	298987	1	
FLA299063	299063	1	
FLA299772	299772	1	
FLA299843	299843	1	
FLA299980	299980	1	
FLA300662	300662	1	
FLA300864	300864	1	
FLA302094	302094	1	
FLA302465	302465	1	

-124-

FLA302524	302524	1		
FLA303769	303769	1		
FLA303796	303796	1		
FLA303957	303957	1		
FLA303967	303967	1		
FLA304170	304170	1		
FLA304334	304334	1		
FLA304512	304512	1		
FLA304583	304583	1		
FLA305089	305089	1		
FLA305505	305505	1		
FLA305678	305678	1		
FLA305956	305956	1		
FLA306447	306447	1		
FLA307155	307155	1		
FLA307165	307165	1		
FLA308514	308514	1		
FLA308527	308527	1		
FLA309851	309851	1		
FLA310657	310657	1		
FLA311122	311122	1		
FLA311248	311248	1		
FLA311737	311737	1		
FLA312038	312038	1		
FLA312056/SG13S30	312056	1		
FLA314500	314500	1		
FLA314532	314532	1		
FLA315014	315014	1		
FLA315232	315232	1		
FLA315355	315355	1		
FLA315611	315611	1		
FLA316131	316131	1		
FLA316408	316408	1		
FLA316472	316472	1		
FLA316515	316515	1		
FLA316569	316569	1		
FLA316607	316607	1		
FLA316763/SG13S32	316763	1		
FLA317496	317496	1		
FLA317619	317619	1		
FLA317620	317620	1		
FLA317647	317647	1		
FLA317733	317733	1		
FLA317744	317744	1		
FLA317815	317815	1		
FLA318219	318219	1		

FLA319969	319969	1	
FLA320261	320261	1	
FLA320393/SG13S42	320393	1	
FLA320595	320595	1	
FLA321774	321774	1	
FLA321966	321966	1	
FLA322025	322025	1	
FLA322093	322093	1	
FLA323013	323013	1	
FLA323316/SG13S34	323316	1	
FLA323366	323366	1	
FLA324591	324591	1	
FLA324601	324601	1	
FLA324849	324849	1	
FLA325369	325369	1	
FLA326187	326187	1	
FLA326657	326657	1	
FLA327265	327265	1	
FLA328964	328964	1	
FLA330265	330265	1	
FLA330455	330455	1	
FLA331234	331234	1	
FLA331374	331374	1	
FLA331395	331395	1	
FLA331473	331473	1	
FLA331517	331517	1	
FLA331526	331526	1	
FLA331651	331651	1	
FLA331841	331841	1	
FLA287889/DG00AAJFF	287889	1	
DG00AAFIU/SNP_13_Y1323892	256047	1	
SG13S35/FLA324333	324333	1	
SG13S86	305031	1	
* indicates a publicly available SNP.			

Table 4

Significant 4 microsatellite marker haplotypes. Length=length of haplotype in Mb. P-val=p-value. RR=Relative risk. N af=Number of patients. P al=allelic frequency of haplotype. P ca=carrier frequency of haplotype. N ct= number of controls. Alleles= alleles in the haplotype. Markers= markers in the haplotype.

4 markers	Length	p-val	RR	N af	P al	P ca	N ct	P al	P ca	Alleles	Markers
	0.88	4.71E-06	6.23	428	0.065	0.125	721	0.011	0.022	0 -12 -6 0	DG13S80 DG13S83 DG13S1110 DG13S163
	0.82	8.60E-06	INF	438	0.032	0.062	720	0	0	0 4 2 14	DG13S111 1 DG13S1103 D13S1287 DG13S1061
	0.67	6.98E-06	19.91	435	0.03	0.059	721	0.002	0.003	8 6 0 8	DG13S1103 DG13S163 D13S290 DG13S1061
	0.767	4.85E-06	26.72	436	0.048	0.094	721	0.002	0.004	0 0 2 12	DG13S1101 DG13S166 D13S1287 DG13S1061
	0.515	1.93E-06	INF	422	0.048	0.094	721	0	0	2 0 0 6	DG13S166 DG13S163 D13S290 DG13S1061
	0.864	1.68E-06	INF	424	0.024	0.048	717	0	0	0 2 0 -16	DG13S166 DG13S163 DG13S1061 DG13S293
	0.927	5.38E-06	INF	435	0.034	0.067	720	0	0	4 2 14 3	DG13S1103 D13S1287 DG13S1061 DG13S301

Alleles #'s: For SNP alleles A = 0, C = 1, G = 2, T = 3; for microsatellite alleles: the CEPH sample (Centre d'Etudes du Polymorphisme Humain, genomics repository) is used as a reference, the lower allele of each microsatellite in this sample is set at 0 and all other alleles in other samples are numbered according in relation to this reference. Thus allele1 is 1 bp longer than the lower allele in the CEPH sample, allele 2 is 2 bp longer than the lower allele in the CEPH sample, allele 3 is 3 bp longer than the lower allele in the CEPH sample, allele 4 is 4 bp longer than the lower allele in the CEPH sample, allele -1 is 1 bp shorter than the lower allele in the CEPH sample, allele -2 is 2 bp shorter than the lower allele in the CEPH sample, and so on.

Table 5

Significant 5 microsatellite marker haplotypes. Length=length of haplotype in Mb. P-val=p-value. RR=Relative risk. N af=Number of patients. P al=allelic frequency of haplotype. P ca =carrier frequency of haplotype. N ct= number of controls. Alleles= alleles in the haplotype. Markers= markers in the haplotype

5markers	Length	p-val	RR	N af	P al	P ca	N ct	P al	P ca	Alleles	Markers
	0.851	7.45E-06	15.43	413	0.034	0.067	715	0.002	0.005	0 18 0 0 0	DG13S79 D13S1299 DG13S87 D13S1246 DG13S166
	0.964	8.07E-06	INF	437	0.023	0.045	721	0	0	0 -12 6 8 6	DG13S79 DG13S83 DG13S1104 DG13S1103 DG13S163
	0.964	2.38E-06	INF	437	0.026	0.052	720	0	0	0 6 0 8 6	DG13S79 DG13S1104 DG13S172 DG13S1103 DG13S163
	0.931	7.05E-06	5.8	429	0.068	0.131	721	0.012	0.025	0 -6 0 0 -2	DG13S79 DG13S1110 DG13S175 DG13S166 D13S1238
	0.964	8.13E-06	INF	434	0.021	0.041	721	0	0	0 3 8 2 6	DG13S79 DG13S1098 DG13S1103 DG13S166 DG13S163
	0.597	9.78E-06	4.58	428	0.074	0.143	717	0.017	0.034	-6 0 0 0 -2	DG13S1110 DG13S89 DG13S175 DG13S166 D13S1238
	0.896	6.92E-06	INF	428	0.026	0.051	721	0	0	-12 -6 0 -2 2	DG13S83 DG13S1110 DG13S166 D13S1238 D13S290
	0.722	2.18E-06	INF	453	0.026	0.051	738	0	0	-6 0 0 -2 2	DG13S1110 D13S289 DG13S166 D13S1238 D13S290
	0.982	7.88E-06	INF	437	0.028	0.055	721	0	0	0 0 4 2 14	DG13S87 DG13S175 DG13S1103 D13S1287 DG13S1061
	0.841	8.88E-06	INF	438	0.032	0.062	720	0	0	0 0 4 2 14	DG13S89 DG13S1111 DG13S1103 D13S1287 DG13S1061

-128-

0.841	9.67E-07	INF	435	0.029	0.057	721	0	0	0	8	6	0	8	DG13S89 DG13S1103 DG13S163 D13S290 DG13S1061
0.982	7.90E-06	18.63	437	0.026	0.052	721	0.001	0.003	0	4	0	2	14	DG13S87 DG13S1103 DG13S166 D13S1287 DG13S1061
0.841	3.52E-06	28.52	436	0.048	0.094	721	0.002	0.004	0	0	0	2	12	DG13S89 DG13S1101 DG13S166 D13S1287 DG13S1061
0.705	5.28E-06	INF	435	0.027	0.053	721	0	0	0	8	6	0	8	DG13S175 DG13S1103 DG13S163 D13S290 DG13S1061
0.841	4.21E-06	INF	422	0.048	0.093	721	0	0	0	2	0	0	6	DG13S89 DG13S166 DG13S163 D13S290 DG13S1061
0.767	4.02E-06	28.11	436	0.049	0.095	721	0.002	0.004	0	0	0	2	12	DG13S1101 DG13S175 DG13S166 D13S1287 DG13S1061
0.767	1.29E-06	31.07	436	0.047	0.092	721	0.002	0.003	0	0	0	2	12	DG13S1101 DG13S172 DG13S166 D13S1287 DG13S1061
0.705	4.25E-07	INF	422	0.048	0.093	721	0	0	0	2	0	0	6	DG13S175 DG13S166 DG13S163 D13S290 DG13S1061
0.683	6.58E-06	INF	437	0.029	0.056	721	0	0	0	4	0	2	14	DG13S172 DG13S1103 DG13S166 D13S1287 DG13S1061
0.767	2.85E-06	32.43	436	0.044	0.087	721	0.001	0.003	0	0	0	2	12	DG13S1101 DG13S166 D13S290 D13S1287 DG13S1061
0.865	9.58E-06	18.39	451	0.023	0.045	739	0.001	0.003	0	0	2	2	16	D13S289 DG13S166 DG13S163 D13S1287 DG13S293
0.865	5.08E-06	INF	453	0.019	0.038	739	0	0	0	0	2	0	16	D13S289 DG13S166 DG13S163 DG13S1061 DG13S293
0.927	1.02E-07	27.65	437	0.037	0.073	721	0.001	0.003	4	0	2	14	3	DG13S1103 DG13S166 D13S1287 DG13S1061 DG13S301

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[illegible]

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[illegible]

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Table 8 The frequencies of the female MI "at risk" haplotypes in male patients vs controls.

10	DG13S1103	DG00AAFQR	SNP13B_R1028729	SNP13B_Y1323898	SNP13B_K912392	DG00AAFIV	D13S289	DG13S168	DG00AAFJT	DG00AAHII	DG00AAHID	DG00AAHIJ	DG00AAHIH	DG00AAHIE	B_SNP_302524	B_SNP_302617	DG00AAHIG	DG00AAHIF	DG00AAHOI	D13S1238	DG13S2605	DG13S163	p-val	N_aff	aff.frq	N_ctl	ctl.frq	rel_risk	PAR	Info
15	male MI	0																												
	p-val: p-value for the association. N_aff: Number of patients used in the analysis. Aff.frq: haplotype frequency in patients. N_ctl: number of controls used in the analysis. Ctl.frq: Haplotype frequency in controls. Rel_risk: Relative risk of the haplotype. PAR: population attributable risk. Info: information content.																													
																							3.39E-01	1087	0.027	809	0.024	1.32	0.013	0.577
																						3.39E-01	1087	0.056	809	0.05	1.13	0.013	0.568	

Table 9. The selected SNP haplotypes and the corresponding p-values, relative risk (RR), number of patients (#aff), allelic frequency in patients (aff.frq.), carrier frequency in patients (carr.frq.), number of controls (#con), allelic frequency in controls (con.frq.), population attributable risk (PAR). The patients used for this analysis were all unrelated within 4 meioses.

	p-val	RR	#aff	aff.frq.	carr.frq.	#con	con.frq.	PAR	DG00AAFIU	SG13S25	DG00AAJFF	DG00AAHII	DG00AAHID	B_SNP_310657	SG13S30	SG13S32	SG13S42	SG13S35
B4	4.80E-05	2.08	903	0.106	0.2	619	0.054	0.11		2		2			2		0	
B5	2.40E-05	2.2	910	0.101	0.19	623	0.049	0.11	3	2		2			2		0	
B6	1.80E-06	2.22	913	0.131	0.24	623	0.063	0.14	3	2	2	2				0		2
A4	5.10E-06	1.81	919	0.159	0.29	623	0.095	0.14		2			3	2		0		
A5	2.60E-06	1.91	920	0.15	0.28	624	0.085	0.14	3	2			3	2		0		

EXAMPLE 2 RELATIONSHIP BETWEEN MUTATION IN 5-LO PROMOTER AND MI

A family of mutations in the G-C rich transcription factor binding region of the 5-LO gene has previously been identified. These mutations consist of deletion of one, deletion of two, or addition of one zinc finger (Sp1/Egr-1) binding sites in the region 176 to 147 bp upstream from the ATG translation start site where there are normally 5 Sp1 binding motifs in tandem. These naturally occurring mutations in the human 5-LO gene promoter have been shown to modify transcription factor binding and reporter gene transcription. The capacity of the mutant forms of DNA to promote transcription of CAT reporter constructs have been shown to be significantly less than that of the wild type DNA (*J. Clin. Invest.* Volume 99, Number 5, March 1997, 1130-1137).

To test whether 5-LO is associated with the atherosclerotic diseases, particularly myocardial infarction (MI) in the human population, this promoter polymorphism, consisting of variable number of tandem Sp1/Egr-1 binding sites, was genotyped in 1112 MI patients, 748 patients with PAOD, and 541 stroke patients.

The results, shown in Table 10, demonstrate that the wild type allele (which represents the allele with the most active promoter and thus with the highest expression of the 5-LO mRNA) is significantly associated with MI (RR=1.2, $p<0.05$). The results are consistent with a disease hypothesis that increased expression of the 5-LO plays a role in the pathogenesis of MI.

Table 10

	N_aff	Frq_aff	N_ctrl	Frq_ctrl	Risk Ratio	P-value
MI patients	1112	0.8701	734	0.8501	1.1803	0.048
Independent	969	0.8720	734	0.8501	1.2013	0.037
Males	646	0.8740	734	0.8501	1.2232	0.039
Females	465	0.8645	734	0.8501	1.1249	0.180
Age of onset < 60	522	0.8745	734	0.8501	1.2286	0.046
Males	353	0.8768	734	0.8501	1.2542	0.053
Females	169	0.8698	734	0.8501	1.1779	0.202

EXAMPLE 3: ELEVATED LTE4 BIOSYNTHESIS IN INDIVIDUALS WITH THE FLAP MI-RISK HAPLOTYPE

Based on the known function of the end products of the leukotriene pathway and based on our 5-LO association data, the association of the FLAP haplotype with MI is best explained by increased expression and/or increased function of the FLAP gene. In other words, those individuals that have a "at risk" FLAP haplotype have either, or both, increased amount of FLAP, or more active FLAP. This would lead to increased production of leukotrienes in these individuals.

10 To demonstrate this theory, LTE4, a downstream leukotriene metabolite, was measured in patient serum samples. A quantitative determination of LTE4 in human serum was performed by liquid chromatography coupled with tandem mass spectrometry. The protocol was performed as follows:

ANALYTICAL METHOD

Table P1 (Protocol 1): List of Abbreviations

5

CAN	Acetonitrile
IS	Internal standard
LC-MS/MS	Liquid chromatography tandem mass spectrometry
LOQ	Limit of quantification
QCs	Quality controls
R ²	Coefficient of determination
SS	Spiking solution

Apparatus and conditions

Table P2 Analytical apparatus and conditions

Instruments / Conditions	Details																												
Analytical column	Zorbax extend C ₁₈ , 3.5µm (50 x 2.1 mm)																												
Column temperature	Ambient																												
Pump and flow	Hewlett Packard Series 1100 Binary pump delivering 0.3 ml/min																												
Mobile phase	A: Buffer: Acetonitrile:H ₂ O (5:95 % v/v). (Containing 10 mM Ammonium Acetate and 0.1% Acetic acid at pH 4.6). B: Buffer: Acetonitrile:H ₂ O (95:5 % v/v). (Containing 10 mM Ammonium Acetate and 0.1% Acetic acid at pH 4.6).																												
Gradient	<table><tr><th>Time</th><th>%A</th><th>%B</th><th>Flow rate</th></tr><tr><td>0.00</td><td>30</td><td>70</td><td>0.3 ml/min</td></tr><tr><td>1.00</td><td>30</td><td>70</td><td>0.3 ml/min</td></tr><tr><td>1.50</td><td>90</td><td>10</td><td>0.3 ml/min</td></tr><tr><td>6.00</td><td>90</td><td>10</td><td>0.3 ml/min</td></tr><tr><td>6.50</td><td>30</td><td>70</td><td>0.3 ml/min</td></tr><tr><td>10.00</td><td>30</td><td>70</td><td>0.3 ml/min</td></tr></table>	Time	%A	%B	Flow rate	0.00	30	70	0.3 ml/min	1.00	30	70	0.3 ml/min	1.50	90	10	0.3 ml/min	6.00	90	10	0.3 ml/min	6.50	30	70	0.3 ml/min	10.00	30	70	0.3 ml/min
Time	%A	%B	Flow rate																										
0.00	30	70	0.3 ml/min																										
1.00	30	70	0.3 ml/min																										
1.50	90	10	0.3 ml/min																										
6.00	90	10	0.3 ml/min																										
6.50	30	70	0.3 ml/min																										
10.00	30	70	0.3 ml/min																										
Sample injection	HTC PAL autosampler 10 µl onto the HPLC column																												
Mass Spectrometric system	Quattro Ultima™ Tandem MS/MS, Micromass. England.																												
Recording and integration	Mass Lynx, version 3.5. All chromatograms and reports are printed out in hardcopy and stored in electronic form on the workstation hard disk drive. Recording time was 10 min.																												
Retentions times	LTE ₄ ~ 3.05 min. LTE ₄ -d ₃ ~ 3.05 min.																												
Ionization mode	Electrospray atmospheric pressure in negative ion mode																												

-135-

Scan mode	Multiple reaction monitoring (MRM)		
	Compound	Parent ion	Daughter ion
	LTE ₄	438.2	333.2
	LTE ₄ -d ₃	441.2	336.2

Other instruments

Table P3 The apparatus used for sample treatment and measurements

Apparatus	Brand	Type
Pipette	Eppendorf	Edos 5221
Pipette	Labsystems	Finnpipette 200 µl
Centrifuge	Eppendorf	5417C
Evaporation unit	Porvair	Ultravap
Vibrofix	Ika-Werk	VF-1
	Thermolyne	Maxi-mix III TM , 65800
Balance	Sartorius	LA 120 S
Ultra sonic bath	Cole Parmer	8891

Materials

5 Table P4 Reagents for sample treatment and measurements

Reagent	Manufacturer	Quality	Art no.
Acetonitrile (ACN)	Rathburn	HPLC grade	RH 1016
Methanol	Rathburn	HPLC grade	RH 1019
Ammonium acetate	Merck	Pro analysis	1116

Table P5 Reference substances

	Details	Reference
Reference standards	Leukotrine E ₄ from Cayman Chemical, MI, USA	20410
Internal standards	Leukotriene E ₄ -20, 20,20-d ₃ from Biomol, PA, USA	S10120

Stock solutions

A stock solution of LTE₄ was prepared by the supplier at a concentration of 100 µg/ml in methanol. The stock solution was diluted to a concentration of 20 µg/ml in methanol and this working solution (WS-1) was kept refrigerated at 2-8°C.

An internal standard stock solution (LTE₄-d₃) was prepared by the supplier at a concentration of 49.5 µg/ml. The stock solution was diluted to a concentration of 1 µg/ml in methanol and this working solution was kept refrigerated at 2-8°C.

Preparation of spiking solutions, calibration standards and quality control samples

Spiking solutions (SS) in the concentration range of 1 ng/ml to 10000 ng/ml were prepared by dilution of the working Solution.

The following spiking solutions were prepared:

Table P6 Spiking solutions for calibration standards

SS	Concentration (ng/ml)	Preparation
1	10000	500 µl of WS-1 (20 µg/ml) diluted to 1.0 ml with 70% MeOH/water
2	1000	100 µl of SS-1 was diluted to 1.0 ml with 70% MeOH/water
3	100	100 µl of SS-2 was diluted to 1.0 ml with 70% MeOH/water
4	30	300 µl of SS-3 was diluted to 1.0 ml with 70% MeOH/water
5	20	200 µl of SS-3 was diluted to 1.0 ml with 70% MeOH/water

-137-

6	16	160 μ l of SS-3 was diluted to 1.0 ml with 70% MeOH/water
7	12	120 μ l of SS-3 was diluted to 1.0 ml with 70% MeOH/water
8	8.0	400 μ l of SS-5 was diluted to 1.0 ml with 70% MeOH/water,
9	4.0	200 μ l of SS-5 was diluted to 1.0 ml with 70% MeOH/water
10	2.0	100 μ l of SS-5 was diluted to 1.0 ml with 70% MeOH/water
11	1.4	175 μ l of SS-8 was diluted to 1.0 ml with 70% MeOH/water
12	1.0	125 μ l of SS-8 was diluted to 1.0 ml with 70% MeOH/water

Table P7 Spiking solutions for quality controls

SS	Concentration (ng/ml)	Preparation
13	14	140 μ l of SS-3 was diluted to 1.0 ml with 70% MeOH/water
14	6.0	300 μ l of SS-5 was diluted to 1.0 ml with 70% MeOH/water
15	2.4	120 μ l of SS-5 was diluted to 1.0 ml with 70% MeOH/water

After preparation, spiking solutions for calibration standards and quality
5 controls were kept refrigerated at 2-8°C.

Preparation of calibration standards and quality controls

Fresh calibration standards and quality controls (QCs) were prepared each day by spiking blank plasma as described in Tables P8 and P9, respectively.

Table P8 Preparation of calibration standards

Concentration (ng/ml)	SS (μ l)	Blank Plasma
1500	20 μ l of the SS-4 (30ng/ml)	380 μ l
1000	20 μ l of the SS-5 (20ng/ml)	380 μ l
800	20 μ l of the SS-6 (16ng/ml)	380 μ l
600	20 μ l of the SS-7 (12ng/ml)	380 μ l
400	20 μ l of the SS-8 (8ng/ml)	380 μ l
200	20 μ l of the SS-9 (4.0ng/ml)	380 μ l
100	20 μ l of the SS-10 (2.0ng/ml)	380 μ l
70	20 μ l of the SS-11 (1.4ng/ml)	380 μ l
50	20 μ l of the SS-12 (1.0ng/ml)	380 μ l

Table P9 Preparation of quality controls

Concentration (ng/ml)	SS (μ l)	Blank Plasma
800	20 μ l of the SS-13 (14ng/ml)	380 μ l
40	20 μ l of the SS-14 (6.0ng/ml)	380 μ l
8.0	20 μ l of the SS-15 (2.4ng/ml)	380 μ l

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Sample preparation

Aliquots of 400 μ l of each study sample, calibration standards, QC samples and control blank are pipetted into an eppendorf vial. All samples apart from blank are then spiked with 20 μ l of internal standard working solution and the samples are then vortex-mixed for few seconds. The pH of the plasma samples is adjusted to pH 4.5 using 60 μ l of 10% acetic acid and centrifuged for 10 min. at 4100 rpm immediately before the extraction. The solid phase extraction 96-well plate is

conditioned with 1 ml methanol and 1 ml water. Then 400 μ l of the plasma samples are loaded on the plate. Vacuum is applied, followed by drying the disk for 1 min. After being washed with 2ml water and 1 ml 30% methanol in 2% acetic acid. Next the plate is eluted with 0.6 ml methanol. The plate is then dried for few minutes. The
5 methanol eluate is evaporated almost to dryness under a stream of nitrogen at 45°C. The residue is reconstituted in 30 μ l mobile phase and vortex-mixed for few min. Subsequently, the solutions are centrifuged for 10 min at 10.000 rpm. and 10 μ l are injected by the autosampler into the LC-MS/MS system for quantification.

10 *PERFORMANCE OF MEASUREMENTS*

The samples will be prepared and measured in batches and a typical batch will consist of:

- 15 One set of calibration standards, one extra lowest calibration standard and one blank.
Samples collected from a 16 individuals and one set of control samples (C_L , C_M , C_H)
Samples collected from a 17 individuals and one set of control samples (C_L , C_M , C_H)

QUANTITATIVE DETERMINATION OF ANALYTE IN PLASMA SAMPLES

20 The standard curve is calculated from the peak area ratios ANALYTE/INTERNAL STANDARD of the calibration standards and their nominal ANALYTE concentrations. The unknown samples for LTE₄ were calculated from a quadratic regression equation where a weighted curve, $1/X^2$, is used. The measured peak area of the samples was converted into pictogram of ANALYTE per milliliter
25 (pg/ml) of plasma according to the calculated equation for the standard curve.

The calculation of the regression for the standard curve and the calculations of the concentration of the unknown samples and the control samples are performed with MassLynx Software.

ACCEPTANCE CRITERIA

Calibration standards

The coefficient of determination (R^2) for the calibration curve must exceed 0.98.

- 5 The calibration curve included the concentration range from 50pg/ml – 1500pg/ml.

Concentration of the calibration standards must be within $\pm 25\%$ of their nominal value when recalculated from the regression equation. Calibration standards that fail these criteria (at most 3 in each run) are rejected and the calibration performed again
10 with the remaining standards. If the standard curve is not accepted, the samples must be reanalyzed.

Control samples

At least two thirds of the analysed quality controls must be within $\pm 25\%$ of their nominal value when calculated from regression equation. If more than a third of
15 the controls fail, the samples must be reanalyzed.

RESULTS

Table 11 (below) shows that the female MI “at risk” haplotype is more significantly associated with female MI patients who have high LTE4 levels (top 50th
20 percentile), than with female MI patients who have low levels of LTE4 (bottom 50th percentile).

In addition, haplotype analysis, comparing female MI patients with high levels of LTE4 with female patients with low levels, showed that those with high levels had increased prevalence of the “at risk” haplotype by 1.6 fold (see Table 12). The results
25 show clearly that the “at risk” haplotypes are enriched in the MI patient group that has high levels of LTE4. The carrier frequency of the “at risk” haplotypes are 12% and 20%, respectively, in the whole female MI group, but go up to 15% and 24%, respectively, in the female MI group that has high levels of LTE4. Correspondingly, the carrier frequency of the “at risk” haplotypes decrease to 8% and 18%,

-141-

respectively, in the group of female MI that has low levels of LTE4 (Note carrier frequencies are twice the disease allele frequency times 1 minus the disease allele frequency plus the square of the disease allele frequency).

Note that LTE4 may simply reflect the leukotriene synthesis rate of the leukotriene synthetic pathway upstream of the key leukotriene metabolite involved in MI risk. For example, leukotriene B4 is probably more likely than leukotriene E4 to be involved in the inflammatory aspects of MI plaques but since B4 has a short half life, it is difficult to measure reliably in serum samples, while E4 has long term stability.

Table 11 Association of the at risk haplotypes for female MI, with female MI who also have high levels of LTE4 (>50pg/ml (roughly the upper 50th percentile). Less significant association between the at risk haplotype for female MI, with female MI who also have low levels of LTE4 (<50pg/ml).

15		DG13S103	DG00AAFQR	SNP13B_R1028729	SNP13B_Y1323898	SNP13B_K912392	DG00AAFIV	D13S289	DG13S166	DG00AAFJT	DG00AAHIJ	DG00AAHID	DG00AAHIJ	DG00AAHIH	DG00AAHIE	B_SNP_302524	B_SNP_302617	DG00AAHIG	DG00AAHIF	DG00AAHOI	D13S1238	DG13S2605	DG13S163																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							</
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P-val: p-value for the association. N_aff: Number of patients used in the analysis. Aff. frq: haplotype frequency in patients. N_ctrl: number of controls used in the analysis. Ctrl.frq: Haplotype frequency in controls. Rel_risk: Relative risk of the haplotype. PAR: population attributable risk. Info: information content.

Table 12 Association between haplotypes that are most significantly associated with female MI, and serum LTE4 levels. Here, the group of affected individuals are defined as female MI patients with high serum LTE4 (higher than 50 pg/ml) and the control group is defined as female MI patients with low serum LTE4

5 (below 50 pg/ml)

10		DG13S1103	DG00AAFQR	SNP13B_R1028729	SNP13B_Y1323898	SNP13B_K912392	DG00AAFIV	D13S289	DG13S166	DG00AAFJT	DG00AAHII	DG00AAHID	DG00AAHIJ	DG00AAHIH	DG00AAHIE	B_SNP_302524	B_SNP_302817	DG00AAHIG	DG00AAHIF	DG00AAHOI	D13S1238	DG13S2605	DG13S163		p-val	N_aff	aff.frq	N_ctrl	ctrl.frq	rel_risk	PAR	Info					
15		High vs low LTE4																																			
		0		1		3		0				3					3			2	-2			1.61E-01	221	0.084	185	0.054	1.61	0.063	0.689						
				1		3		0												2	-2			1.20E-01	220	0.13	182	0.088	1.54	0.089	0.686						

P-val: p-value for the association. N_aff: Number of patients used in the analysis. Aff. frq: haplotype frequency in patients.
 20 N_ctrl: number of controls used in the analysis. Ctrl.frq: Haplotype frequency in controls. Rel_risk: Relative risk of the haplotype. PAR: population attributable risk. Info: information content.

EXAMPLE 4 ELEVATED LTE4 CORRELATED WITH ELEVATED C-REACTIVE PROTEIN (CRP)

30 The relationship between the increased production of leukotrienes and the inflammatory marker CRP, a well established risk factor for MI, was then explored. As shown in FIG. 9, a significant positive correlation was found between serum LTE4 levels and serum CRP levels.

EXAMPLE 5: ASSESSMENT OF LEVEL OF CRP IN PATIENTS WITH AT-RISK HAPLOTYPE

35 The level of CRP in female patients with female MI at-risk haplotypes was assessed, in order to demonstrate the presence of a raised level of inflammatory
 40 marker in the presence of the female MI at-risk haplotype. Results are shown in Table 13. The average CRP was elevated in those patients with the at-risk haplotype versus those without it.

Table 13

All female patients		no	Mean CRP	SE CRP
affecteds:	With haplotype.	155	4.91	8.7
	Not with haplotype.	218	4.35	6.13

5
EXAMPLE 6: ELEVATED SERUM LTE4 LEVELS IN MI PATIENTS VERSUS CONTROLS

The end products of the leukotriene pathway are potent inflammatory lipid mediators that can potentially contribute to development of atherosclerosis and destabilization of atherosclerotic plaques through lipid oxidation and/or proinflammatory effects. Examples one through five show that: 1) MI correlates with genetic variation at FLAP; 2) MI correlates with high expression promoter polymorphism at 5-LO; 3) C-reactive protein levels correlate with serum leukotriene E4; and 4) Patients with MI-risk FLAP haplotypes have higher levels of serum leukotriene E4 and CRP. Based on these data, it was hypothesized that serum leukotriene E4 levels correlate with MI risk.

To test this hypothesis, LTE4, a downstream leukotriene metabolite, was measured in 488 female MI patient and 164 control serum samples. The LTE4 levels for the patients was higher than that for the controls using a one-sided Wilcoxon rank-sum test. The p-value of the difference was 0.0092 thus confirming our hypothesis. Therefore, elevated leukotriene E4 represents a risk factor for MI. Serum or plasma LTE4 levels may be used to profile the MI risk for individuals to aid in deciding which treatment and lifestyle management plan is best for primary or secondary MI prevention. In the same way other leukotriene metabolites may be used to risk profile for MI.

SUMMARY

In summary, it has been found that: MI correlates with genetic variation at FLAP; MI correlates with high expression promoter polymorphism at 5-LO; patients with female MI at-risk FLAP haplotypes have higher levels of serum LTE4; LTE4 levels correlate with CRP levels in serum; and patients with MI at-risk FLAP haplotypes have elevated CRP.

Taken together, these results show that increased leukotriene synthesis is a risk factor for MI, especially but not only in females, and that this risk is driven in part by variants in FLAP and 5-LO genes and are captured in part by measurement of levels of serum LTE4 and CRP.

MARKERS UTILIZED HEREIN

Table 14: Position (Mb) of microsatellite markers sequence assembly (SA5), primers and size of the markers.

mb	Marker	Forward	Reverse	size
25.0920 42	DG13S2101	ACGGTGATGACGCCTACATT (SEQ ID NO: 4)	TCACATGGACCAATTACCTAGA A(SEQ ID NO: 5)	188
25.0920 42	DG13S48	CAAATTTTCAGATGTGCCAACC (SEQ ID NO: 6)	ACGGTGATGACGCCTACATT(S EQ ID NO: 7)	214
25.3965 04	D13S1304	ACCAGCCTTTGCTTAGGA(SEQ ID NO: 8)	ACATTCTAGTGCTACAGGGTAC TC(SEQ ID NO: 9)	133
25.3965 35	DG13S2105	TGTTCTGCACACGAACATTCT(SE Q ID NO: 10)	TCCTGAGTCCTCTCCACCTG(S EQ ID NO: 11)	104
25.4455 11	DG13S2106	TGGGAATTAATGAAGAACAACAA A(SEQ ID NO: 12)	CATGTTTCGAAGAACTCAAGAG G(SEQ ID NO: 13)	428
25.5449 20	D13S1254	AAATTACTTCATCTTGACGATAAC A(SEQ ID NO: 14)	CTATTGGGGACTGCAGAGAG (SEQ ID NO: 15)	218
25.5449 25	DG13S2107	GGGACTGCAGAGAGCAGAAG (SEQ ID NO: 16)	CAAGAAGGGAAATTCCTACGC (SEQ ID NO: 17)	95
25.5659 56	DG13S55	AGCCAGTGTCCACAAGGAAG (SEQ ID NO: 18)	GAGGGTGAGACACATCTCTGG (SEQ ID NO: 19)	283
25.6057 93	DG13S54	AATCGTGCCTCAGTTCCATC (SEQ ID NO: 20)	CCACCAGGAACAACACACAC (SEQ ID NO: 21)	156
25.6196 93	D13S625	TTGCTCTCCAGCCTGGGC (SEQ ID NO: 22)	TTCTCTGGCTGCCTGCG (SEQ ID NO: 23)	185
25.6874 22	DG13S1479	TTGATTCCGTGGTCCATTA (SEQ ID NO: 24)	TTATTTGGTCGGTGCACCTTT (SEQ ID NO: 25)	339
25.7493 44	DG13S1440	GGTAGGTTGAAATGGGCTAACA (SEQ ID NO: 26)	TCATGACAAGGTGTTGGATTT (SEQ ID NO: 27)	153

-145-

25.9012	12	DG13S1890	CCTCCTCTGCCATGAAGCTA (SEQ ID NO: 28)	CTATTTGGTCTGCGGGTTGT (SEQ ID NO: 29)	418
25.9280	81	DG13S1879	TTTGAGCCCAGATCTAAGCAA (SEQ ID NO: 30)	AAATGTTAATGTCACCGACAAA (SEQ ID NO: 31)	443
25.9326	09	DG13S1540	TACTGGGTTATCGCCTGACC (SEQ ID NO: 32)	CCAATGGACCTCTTGGACAT (SEQ ID NO: 33)	152
25.9467	43	DG13S1889	TTTGAATGTTTCATATATTTGTGGT (SEQ ID NO: 34)	CCCTCGTAATGAAACCTATTTG (SEQ ID NO: 35)	222
25.9486	79	DG13S59	TTTCGGGCACAGTCCTCAATA (SEQ ID NO: 36)	CAGGGTGTGGTGACAT (SEQ ID NO: 37)	228
25.9523	47	DG13S1894	TGTTTCTTTCTTTCTCTCTCTTT (SEQ ID NO: 38)	AAATGAGTTCAATGAGTTGTGG TT (SEQ ID NO: 39)	209
25.9883	60	DG13S1545	CAGAGAGGAACAGGCAGAGG (SEQ ID NO: 40)	AGTGGCTGGGAAGCCTTATT (SEQ ID NO: 41)	394
26.0718	66	DG13S1524	AGGTGAGAGAACAACCTGTCTT (SEQ ID NO: 42)	GCCTTCCTTCTAAGGCCAAC (SEQ ID NO: 43)	115
26.1834	92	DG13S1491	TGTTATACATTTCAATTTACCTC (SEQ ID NO: 44)	GTAATCCAGCCGGGCAAC (SEQ ID NO: 45)	286
26.2362	89	DG13S62	TTGTTCAAGTGCTCTATAGTTACAA AGT (SEQ ID NO: 46)	GGTCACAAAGCTATGCGATTA (SEQ ID NO: 47)	158
26.2734	63	D13S1244	TCAACAAGTGGATTAAGAACTG TG (SEQ ID NO: 48)	CTGTTTATGGCTGAGAAGTATG C (SEQ ID NO: 49)	86
26.2869	35	DG13S64	TAGCAGGGTGCAGTCTA (SEQ ID NO: 50)	ACCATACCACCACCACCATC (SEQ ID NO: 51)	247
26.3145	01	D13S243	ACTGTACTTCTGCCTGGGC (SEQ ID NO: 52)	TTTGTGAATGCCTCAACCATG (SEQ ID NO: 53)	147
26.3271	84	DG13S1529	CTGTAGACTTTATCCCTGACTTAC TG (SEQ ID NO: 54)	CAATGAATGATGAAGATTCCAC TC (SEQ ID NO: 55)	132
26.3387	67	DG13S1908	TGACACCATGTCTTACTGTTTGC (SEQ ID NO: 56)	GAGGATACAATGAGAACCAAAT CTC (SEQ ID NO: 57)	224
26.3880	34	DG13S1546	CCACAGAATGCTCCAAAGGT (SEQ ID NO: 58)	GAGTTCAAGTGATGGATGACG A (SEQ ID NO: 59)	357
26.4358	11	DG13S1444	CAGATAGATGAATAGGTGGATGG A (SEQ ID NO: 60)	CACTGTTCCAAGTGCTTTGC (SEQ ID NO: 61)	193
26.4866	57	DG13S1458	GCAGGGCAAACCTGCCTTAT (SEQ ID NO: 62)	TTTGGTGAAATGTCTGTTTATG G (SEQ ID NO: 63)	402
26.5045	45	D13S252	CTCAACCTGGCTTCTACT (SEQ ID NO: 64)	TACTCCTTAATAAACTCCCC (SEQ ID NO: 65)	338
26.5082	31	DG13S66	TATGCGTTGTGTGTGTG (SEQ ID NO: 66)	GGGCCTTAGATTCTTGTAGTG G (SEQ ID NO: 67)	217
27.1151	20	DG13S1554	CTCGCATCTCGCTTCTCACT (SEQ ID NO: 68)	CTCAAGGGTCCAGTGGTTTG (SEQ ID NO: 69)	420
27.1406	75	DG13S1907	TGTCCAGACTGCCTCCTACA (SEQ ID NO: 70)	TGCAACACCTGGTTCACAAT (SEQ ID NO: 71)	131
27.1458	42	D13S802	CACAGTGAGACTCTATCTCAAAA A (SEQ ID NO: 72)	TCAGACTGGCTTAGACTGTGG (SEQ ID NO: 73)	150
27.2406	16	DG13S1892	AAATTCCAAAGGCCAGGTG (SEQ ID NO: 74)	CCATACAGTTTCCTAGGTTCTG G (SEQ ID NO: 75)	373
27.2534	52	DG13S1849	CACCTGGCCAAATGTTTGT (SEQ ID NO: 76)	TGCTTGAATCCAGAGACTGC (SEQ ID NO: 77)	190
27.2738	60	DG13S68	TTTGCGAGTCCTTGTGGAGT (SEQ ID NO: 78)	ACAGTCCGCTCCCTCCTAAT (SEQ ID NO: 79)	238
27.2804	61	DG13S69	ATGCTTGGCCCTCAGTTT (SEQ ID NO: 80)	TTGGCAACCCAAGCTAATATG (SEQ ID NO: 81)	296

27.4837 99	D13S1250	CTCCACAGTGACAGTGAGG (SEQ ID NO:82)	GAGAGGTTCCCAATCCC (SEQ ID NO: 83)	160
27.6104 06	D13S1448	CATCAACCTCCCCACCAC (SEQ ID NO: 84)	TATTTTTTCAGTCCCACAGTTA GC (SEQ ID NO:85)	227
27.6158 14	DG13S574	CAGCTCCTGGCCATATTTCT (SEQ ID NO: 86)	GAGCCATTTCTCTGGGTCTG (SEQ ID NO:87)	153
27.6412 11	DG13S73	GGTCCGTGTCAACCCTTAGA (SEQ ID NO: 88)	CAGGTTGATGGGAGGGAAA (SEQ ID NO: 89)	198
27.6615 07	DG13S1532	CGGGAAATGACAGTGAGACC (SEQ ID NO: 90)	TGCCTAGATTCTCCCGTAAG (SEQ ID NO: 91)	163
27.7053 47	D13S1242	GTGCCCAGCCAGATTC (SEQ ID NO: 92)	GCCCCCAGTCAGGTTT (SEQ ID NO: 93)	198
27.8838 72	DG13S576	TTTCTCTCTCCACGGAATGAA (SEQ ID NO:94)	AACCCATTCTCACAGGGTGTA (SEQ ID NO: 95)	199
27.8973 65	DG13S1917	AGGAGTGTGGCAGCTTTGAG (SEQ ID NO: 96)	TGGATTCCCGTGAGTACCAG (SEQ ID NO: 97)	165
27.9321 54	D13S217	ATGCTGGGATCACAGGC (SEQ ID NO: 98)	AACCTGGTGGACTTTTGCT (SEQ ID NO: 99)	170
28.0806 32	DG13S581	AGCATTTCCAATGGTGCTTT (SEQ ID NO: 100)	CATGTTGATATGCCTGAAGGA (SEQ ID NO:101)	367
28.1653 48	DG13S1471	CACTGTCTGCTGCCACTCAT (SEQ ID NO:102)	AGAGATTATGTGATGTACCCTC TCTAT (SEQ ID NO:103)	267
28.3032 52	DG13S583	CAAGCCTGGGACACAGAAAT (SEQ ID NO: 104)	TTTGCAGACACCACAACACA (SEQ ID NO: 105)	264
28.3032 56	D13S120	ATGACCTAGAAATGATACTGGC (SEQ ID NO: 106)	CAGACACCACAACACACATT (SEQ ID NO: 107)	175
28.3855 66	D13S1486	TGTTTAAAAACCTCATGCC (SEQ ID NO: 108)	ATCCCCAACTCTGTACTTATGT AGG (SEQ ID NO: 109)	151
28.4155 30	DG13S1024	TTTGCACATACACATAAGCGAAC (SEQ ID NO: 110)	CACAAATCCCGTGCCTAAA (SEQ ID NO: 111)	139
28.4155 30	DG13S1510	ATTCCTGGGCTCATGGTACA (SEQ ID NO: 112)	TGCCGTCATCTGCTTTAGAA (SEQ ID NO: 113)	390
28.4303 08	DG13S1495	CCTTGGCTGTTGTGACTGGT (SEQ ID NO:114)	CACTCAGGTGGGAGGATCAC (SEQ ID NO: 115)	285
28.5175 41	DG13S1482	GCTGTTTCCTTGGCTTCTTCT (SEQ ID NO: 116)	CCCATACTTGAGATGACCATGA (SEQ ID NO: 117)	291
28.5510 60	DG13S1845	CACTTTGCCAGTAGCCTTGA (SEQ ID NO:118)	TTGGGAAAGTTAACCCAGAGA (SEQ ID NO: 119)	284
28.6349 03	DG13S1030	TTTGGGAAGAGCCATGAGAC (SEQ ID NO: 120)	CTCTGGGCATTGGAGGATTA (SEQ ID NO: 121)	354
28.6349 03	DG13S1467	TTTGGGAAGAGCCATGAGAC (SEQ ID NO: 122)	AATGCCCATGTGCACTGTAG (SEQ ID NO: 123)	231
28.6866 07	DG13S584	GGGAGACAAGTCAGGTGAGG (SEQ ID NO: 124)	CTGAGTATGGAGTCTTCATCAT TATC (SEQ ID NO: 125)	151
28.7940 32	DG13S1519	TCGTCTCGAAGAAAGAAAGA (SEQ ID NO:126)	CACCATGGGTTAATTGCACA (SEQ ID NO: 127)	286
28.8761 56	DG13S77	TGACGTGGGTTTCAGGTTGTA (SEQ ID NO: 128)	AGTGCATTGGTGCTTCTCT (SEQ ID NO: 129)	220
28.9707 23	DG13S586	GGACTGCCAATTCTACAGCA (SEQ ID NO: 130)	TTTCATGGGAAATTTGGTC (SEQ ID NO: 131)	151
28.9756 41	DG13S79	TGCTACTAGATTTGACCAACCA (SEQ ID NO: 132)	GACTTGTAAGGATTTAGTGAT TTCG (SEQ ID NO: 133)	128
29.0593 94	DG13S80	GTGGAAGGCCTCTCTTG (SEQ ID NO: 134)	TGCTTCTTGAGGGAAAGCAT (SEQ ID NO: 135)	233

-147-

29.1261	52	DG13S82	CACGTGGTTCACCTCTCTAGG (SEQ ID NO: 136)	TTGGCCACTTATTTGTG (SEQ ID NO: 137)	302
29.1546	91	D13S1299	CGATGAGTGACAGGGCT (SEQ ID NO: 138)	CCTCGTGGGTGGAATAA (SEQ ID NO: 139)	225
29.1547	37	DG13S85	TTGGCCATTAGCAATTAGCA (SEQ ID NO: 140)	CGTGGGTGGAATAAATCAGG (SEQ ID NO: 141)	153
29.1584	62	D13S629	CTTGAGGCAAGAGAATCACT (SEQ ID NO: 142)	GCACATTTACACCAGGGTG (SEQ ID NO: 143)	145
29.2240	60	DG13S1934	CCTTCAGAGGATTTCCCTTTC (SEQ ID NO: 144)	CTGGTTTGACTCCAGCTTCA (SEQ ID NO: 145)	431
29.2454	62	DG13S1098	TGTTCAAACCTAAGGTGCTTCA (SEQ ID NO: 146)	GAAACAACAACAACAACAA CA (SEQ ID NO: 147)	416
29.2598	40	DG13S1104	CCTGGCACGGAATAGACACT (SEQ ID NO: 148)	GGCCTCCTTTGCTCTGAAG (SEQ ID NO: 149)	378
29.2944	36	DG13S1097	CATCCCTGTGGCTGATTAAGA (SEQ ID NO: 150)	AACAGTTCCAGCCCGTTCTA (SEQ ID NO: 151)	162
29.3097	00	DG13S1110	TTTCAAAGGAATATCCAAGTGC (SEQ ID NO: 152)	TGGCGTACCATATAAACAGTTC TC (SEQ ID NO: 153)	265
29.3099	09	DG13S86	TTTCAAAGGAATATCCAAGTGC (SEQ ID NO: 154)	AAACGTGACACTTCCACACA (SEQ ID NO: 155)	177
29.3599	61	DG13S87	TTCAATGAAGGTGCCGAAGT (SEQ ID NO: 156)	TGTCTATCCCAAAGCAA (SEQ ID NO: 157)	218
29.5224	43	DG13S1111	GCAAGACTCTGTTGAAGAAGAAG A (SEQ ID NO: 158)	TCCCTCTGTTTGAGTTTCTCG (SEQ ID NO: 159)	110
29.5746	65	DG13S1101	AGGCACAGTCGCTCATGTC (SEQ ID NO: 160)	AAACTTTAGCTAATGGTGGTCA AA (SEQ ID NO: 161)	333
29.6227	55	DG13S1106	TGTGATTCCAGGGAGCTATCA (SEQ ID NO: 162)	TAGGTGTGTGGAGGACAGCA (SEQ ID NO: 163)	416
29.6589	10	DG13S172	CCAGTTTCAGTTAGCCAAGTCTG (SEQ ID NO: 164)	GAGAGGGAATGAATGCAGGA (SEQ ID NO: 165)	267
29.6657	09	D13S1246	GAGCATGTGTGACTTTCATATTC AG (SEQ ID NO: 166)	AGTGGCTATTCATTGCTACAGG (SEQ ID NO: 167)	177
29.6725	61	DG13S1103	TTGCTGGATGCTGTTTCTA (SEQ ID NO: 168)	AAAGAGAGAGAGAAAGAGAAA GAAAGA (SEQ ID NO: 169)	264
29.8259	75	D13S289	CTGGTTGAGCGGCATT (SEQ ID NO: 170)	TGCAGCCTGGATGACA (SEQ ID NO: 171)	260
29.8266	31	DG13S166	CCTATGGAAGCATAGGGAAGAA (SEQ ID NO: 172)	CCCACTTCTGAGTCTCCTGAT (SEQ ID NO: 173)	395
29.9066	89	DG13S164	GGGATGCAGAAAGGATGTGT (SE Q ID NO: 174)	AAGAATGCTGGCCAACGTAA (S EQ ID NO: 177)	218
29.9067	00	D13S1238	CTCTCAGCAGGCATCCA (SEQ ID NO: 178)	GCCAACGTAATTGACACCA (SE Q ID NO: 179)	129
30.0313	78	D13S290	CCTTAGGCCCCATAATCT (SEQ ID NO: 180)	CAAATTCCTCAATTGCAAAT (S EQ ID NO: 181)	176
30.0863	03	D13S1229	GGTCATTACAGGGAGCCATT (SE Q ID NO: 182)	CCATTATATTTACCAAGAGGC TGC (SEQ ID NO: 183)	119
30.1928	47	DG13S1460	TGCCTGGTCATCTACCCATT (SEQ ID NO: 184)	TCTACTGCAGCGCTGATCTT (S EQ ID NO: 185)	264
30.2176	70	DG13S1933	CATTTATGAATGGAGGTGAAGC (S EQ ID NO: 186)	SATGGGAGCTCAAAGGGAAAT (S EQ ID NO: 187)	186
30.3032	13	DG13S1448	CAGCAGGAAGATGGACAGGT (SE Q ID NO: 188)	CACACTGCATCACACATACCC (SEQ ID NO: 189)	136
30.3178	71	D13S1287	TATGCCAGTATGCCTGCT (SEQ ID NO: 190)	GTCACATCAGTCCATTTGC (SE Q ID NO: 191)	232

-148-

30.3421	02	DG13S1061	CCAAAGCAAGTAACCTCCTCA(SEQ ID NO: 192)	AAACAATCACTGCCCTCTGG(S EQ ID NO: 193)	227
30.5718	37	DG13S1904	TGATGAAATTGCCTAGTGATGC(S EQ ID NO: 194)	GGATCCAATCGTACGCTACC(S EQ ID NO: 195)	136
30.6434	38	DG13S882	CGAATGGGTGACTAACAGCA(SEQ ID NO: 196)	CTGGAGTGCAGGGACATGA(SEQ ID NO: 197)	378
30.6659	37	DG13S295	AAAGAAATATTCCAAGAAGAAAG AAA(SEQ ID NO: 198)	TTGCACAACCTTTGTGTAGAGCA T(SEQ ID NO: 199)	279
30.6744	68	D13S1226	GGGTATGTCTTTATTCTCGGCAG TA(SEQ ID NO: 200)	GTGCATTACAGACCAGTCATT (SEQ ID NO: 201)	219
30.6909	59	DG13S293	GGGCTTGAAGGCACTAAATGT(S EQ ID NO: 202)	CCAAGCAGTAATTCTTCCTCA (SEQ ID NO: 203)	313
30.7124	68	DG13S1490	ACCTAAACACCACGGACTGG(SEQ ID NO: 204)	CAGGTATCGACATTCTTCCAAA (SEQ ID NO: 205)	418
30.8244	83	DG13S93	TGGGAAGCCAGTAAAGTAGGAA(SEQ ID NO: 206)	AAAGAGACTCCACACATCCATT T(SEQ ID NO: 207)	190
30.8248	59	DG13S94	AGGGCTATTCTCAAGGTGTT(SEQ ID NO: 208)	TGCTAACACTACCCTCGCAAT(SEQ ID NO: 209)	332
30.9284	29	DG13S1534	GGGCAGGAATCTCTGAAGTG (SEQ ID NO: 210)	CTCCACTGAGAAGCCAAGGA(S EQ ID NO: 211)	382
30.9403	69	DG13S95	AGGCCAAGCTGGTCCATAG(SEQ ID NO: 212)	TCTCTCAAAGCCTCGCTCTC(S EQ ID NO: 213)	126
30.9702	38	DG13S96	CCTTTGAGGCTGGATCTGTT(SEQ ID NO: 214)	TTTCCTTATCATTATTCCCTCA (SEQ ID NO: 215)	218
31.0388	74	D13S260	AGATATTGTCTCCGTTCCATGA(S EQ ID NO: 216)	CCCAGATATAAGGACCTGGCT A(SEQ ID NO: 217)	163
31.0922	94	DG13S17	TTTAAGCCCTGTGGAATGTATTT(SEQ ID NO: 218)	GACATTGCAGGTCAAGTAGGG(SEQ ID NO: 219)	157
31.2078	44	DG13S306	TGCATAAGGCTGGAGACAGA(SEQ ID NO: 220)	CACAGCAGATGGGAGCAAAA(SEQ ID NO: 221)	158
31.2605	21	DG13S18	GTGCATGTGCATACCAGACC(SEQ ID NO: 222)	GGCAAGATGACCTCTGGAAA(S EQ ID NO: 223)	319
31.2997	20	DG13S1905	GTCCACTGCAGCACACAGAG(SEQ ID NO: 224)	GCACTGGTAGATACATGCTAAC G(SEQ ID NO: 225)	383
31.3532	30	DG13S307	GGGTATCTTGCCAGGTGT(SEQ ID NO: 226)	TGGCTAAGCACAAATCCCTTT(S EQ ID NO: 227)	403
31.3551	35	DG13S1062	TTTGTGTTCCAGGTGAGAATTG(S EQ ID NO: 228)	GAACCATATCCCAAGGCACT(S EQ ID NO: 229)	120
31.4143	29	DG13S1874	AACCCAAATCAACAAACCAGA(SEQ ID NO: 230)	AATGAATTCTGGGTACATGC(SEQ ID NO: 231)	404
31.4295	62	DG13S1093	TTGTTCCCACATTCATTCTACA(S EQ ID NO: 232)	TTAAACTCGTGGCAAAGACG(S EQ ID NO: 233)	273
31.6265	02	DG13S1059	CACCATGCCTGGCTCTTT(SEQ ID NO: 234)	AACTTCTCCAGTTGTGTGGTTG (SEQ ID NO: 235)	330
31.7237	49	DG13S1086	AGCTGAGCTCATGCCACT(SEQ ID NO: 236)	CAAGACCTTGTGCATTTGGA(S EQ ID NO: 237)	155
31.7460	74	DG13S1515	AGCCAGACATGGTAGTGTGC(SEQ ID NO: 238)	GCAATAACTCACACATCAGCAA (SEQ ID NO: 239)	417
31.8557	32	D13S171	CCTACCATTGACACTCTCAG(SEQ ID NO: 240)	TAGGGCCATCCATTCT(SEQ ID NO: 241)	231
31.9173	32	DG13S1092	ACCAAGATATGAAGGCCAAA(SEQ ID NO: 242)	CCTCCAGCTAGAACAATGTGAA (SEQ ID NO: 243)	176
32.0028	52	DG13S1449	TGTCCATAGCTGTAGCCCTGT(SEQ ID NO: 244)	CTCAATGGGCATCTTTAGGC(S EQ ID NO: 245)	279

32.0729	57DG13S1489	TGTAATTCAACGACTGGTGTCC(S	AGCTTCTGATGGTTGCTGGT(S	130
		EQ ID NO: 246)	EQ ID NO: 247)	
32.0839	89DG13S312	CAAACAAACAAACAAGCAAACC(S	TGGACGTTTCTTTCAGTGAGG(349
		EQ ID NO: 248)	SEQ ID NO: 249)	
32.1251	77DG13S1511	TGATAACTTACCAGCATGTGAGC(TCACCTCACCTAAGGATCTGC(314
		SEQ ID NO: 250)	SEQ ID NO: 251)	
32.1835	47DG13S314	CATGCAATTGCCCAATAGAG(SE	TTGGGCTTGTCTACCTAGTTCA	335
		Q ID NO: 252)	(SEQ ID NO: 253)	
32.1953	58DG13S1090	TGGGTTCTCATACTGGAGTG(S	GCCTGAGCTCCAAGCTCTTT(S	169
		EQ ID NO: 254)	EQ ID NO: 255)	
32.2510	38DG13S1071	GCTGCACGTATTTGTTGGTG(SE	AAACAGCAGAAATGGGAACC(S	239
		Q ID NO: 256)	EQ ID NO: 257)	
32.3568	95DG13S1068	CCGTGGGCTATCAATTTCTG(SEQ	AAGATGCAATCTGTTTCCAA(238
		ID NO: 258)	SEQ ID NO: 259)	
32.3730	40DG13S1077	CCAAGACTGAGGAGGTCAA(SE	GCTGACGGAGAGGAAAGAGA(374
		Q ID NO: 260)	SEQ ID NO: 261)	
32.4227	80DG13S1906	TGACAAGGGTGTGGTTATGG	CCGCACTTTCTCTTCTGGAC	425
		(SEQ ID NO: 262)	(SEQ ID NO: 263)	
32.5115	90DG13S316	TGAGAAGCCTGGGCATTAAG	ACAAGCTCATCCAGGGAAAG	243
		(SEQ ID NO: 264)	(SEQ ID NO: 265)	
32.6105	17DG13S317	TTGGAAAGGAAGAAAGGAAGG	TTGAAACCTAAATGCCACCTG	215
		(SEQ ID NO: 266)	(SEQ ID NO: 267)	
32.6107	13DG13S1493	ACCTGTTGTATGGCAGCAGT	GGTTGACTCTTTCCCCAACT	248
		(SEQ ID NO: 268)	(SEQ ID NO: 269)	
32.7898	94DG13S1558	AGAGCTGATCTGGCCGAAG (SEQ	GGTGGACACAGAATCCCACT	399
		ID NO: 270)	(SEQ ID NO: 271)	
32.8659	50DG13S267	GGCCTGAAAGGTATCCTC (SEQ	TCCCACCATAAGCACAAG (SEQ	160
		ID NO: 272)	ID NO: 273)	
32.9614	10DG13S1478	TCAACCTAGGATTGGCATTACA	TCTAGGATTTGTGCCTTTCCA	387
		(SEQ ID NO: 274)	(SEQ ID NO: 275)	
33.0099	22DG13S1513	GACGTCTTAGGATTGACTTCTGC	CCAAATACACATTCTTAAAGGG	173
		(SEQ ID NO: 276)	AAA (SEQ ID NO: 277)	
33.1256	96DG13S1461	GACTGCAGATCGTGGGACTT	TTCTCCAGAGAAACCAAACCA	148
		(SEQ ID NO: 278)	(SEQ ID NO: 279)	
33.1684	68DG13S1551	ATTCGTGCAGCTGTTTCTGC	GCATGACATTGTAAATGGAGG	263
		(SEQ ID NO: 280)	A (SEQ ID NO: 281)	
33.2549	89DG13S1884	GGTGGGAATGTGTGACTGAA	CCAGGTACAACATTCTCCTGAT	123
		(SEQ ID NO: 282)	(SEQ ID NO: 283)	
33.3401	24DG13S1293	TGCAGGTGGGAGTCAA (SEQ ID	AAATAACAAGAAGTGACCTTCC	129
		NO. 284)	TA (SEQ ID NO: 285)	
33.3469	08DG13S326	TGTTCTCCTCACCTGCTCT	TTTCAGGCTAGGAAGATCCTTT	261
		(SEQ ID NO: 286)	(SEQ ID NO: 287)	
33.3926	29DG13S1518	AAAGGATGCATTCGGTTAGAG	ACTGTCCTGTGCCTGTGCTT	375
		(SEQ ID NO: 288)	(SEQ ID NO: 289)	
33.4055	27DG13S23	CCTGAATAGGTGGAATTAAGATC	TCAAGGAGCATACACACACAC	107
		AA (SEQ ID NO: 290)	A (SEQ ID NO: 291)	
33.4315	36DG13S620	GTCCACCTAATGGCTCATTC	CAAGAAGCACTCATGTTTGTG	185
		(SEQ ID NO: 292)	(SEQ ID NO: 293)	
33.4370	92DG13S1866	AGCCTGTGATTGGCTGAGA (SEQ	GGCTTACAGCTGCCTCCTTT	410
		ID NO: 294)	(SEQ ID NO: 295)	
33.4957	18DG13S1927	CCCACAGAGCACTTTGTTAGA	GCCTCCCTTAAGCTGTTATGC	401
		(SEQ ID NO: 296)	(SEQ ID NO: 297)	
33.5034	40DG13S1503	CACTCTTACTGCCAATCACTCC	GCCGTGTGGGTGTATGAAT	226
		(SEQ ID NO: 298)	(SEQ ID NO: 299)	

-150-

33.5681 00	DG13S332	TTGTACCAGGAACCAAAGACAA (SEQ ID NO: 300)	CACAGACAGAGGCACATTGA (SEQ ID NO: 301)	176
33.6758 41	DG13S333	GCTCTGGTCACTCCTGCTGT (SEQ ID NO: 302)	CATGCCTGGCTGATTGTTT (SEQ ID NO: 303)	446
33.7713 89	D13S220	CCAACATCGGGAAGT (SEQ ID NO: 304)	TGCATTCTTTAAGTCCATGTC (SEQ ID NO: 305)	191
33.8180 41	DG13S1919	CAGCAACTGACAACTCATCCA (SEQ ID NO: 306)	CCTCAATCCTCAGCTCCAAC (SEQ ID NO: 307)	255
33.8736 14	DG13S1439	TCCTTCACAGCTTCAAACCTCA (SEQ ID NO: 308)	AGTGAGAAGCTTCCATACTGGT (SEQ ID NO: 309)	239
33.9060 65	DG13S335	GCCAACCGTTAGACAAATGA (SEQ ID NO: 310)	CTACATGTGCACCACAACACC (SEQ ID NO: 311)	201
33.9286 53	DG13S340	AGTTTATTGCCGCCGAGAG (SEQ ID NO: 312)	ACCCACCACATTCCACAAGC (SEQ ID NO: 313)	373
34.0194 55	DG13S1496	CGATTGCCATGTCTCTTTGA (SEQ ID NO: 314)	GAGATCTGGCCTGGATTGT (SEQ ID NO: 315)	155
34.0340 89	DG13S342	TGAGGCCAGCCTTACCTCTAT (SEQ ID NO: 316)	CCAGACATGGTGGCTTGT (SEQ ID NO: 317)	366
34.0617 77	DG13S344	GAAGGAAGGAAGGGAAGGAA (SEQ ID NO: 318)	AAGGATGAGAAGAGTCCATGC (SEQ ID NO: 319)	292
34.0672 39	DG13S345	AAATACCCTTTGAACAGACACAC (SEQ ID NO: 320)	TAGCTGAGCATGGTGGTACG (SEQ ID NO: 321)	201
34.0778 74	DG13S346	AAAGACAAGACAGCAATCCAAA (SEQ ID NO: 322)	GCAGAACCCAGGCTACAGAT (SEQ ID NO: 323)	152
34.0841 38	DG13S347	TCATTGTCAGCACAGAATGAAC (SEQ ID NO: 324)	GGAGGGAGGGGAAGAAAGAGA (SEQ ID NO: 325)	338
34.0843 26	D13S624	GCAACACAGTGAAAGCCCA (SEQ ID NO: 326)	ACAGGAGCATGCCACCATG (SE Q ID NO: 327)	191
34.1560 75	DG13S339	GGGAAGAGGAGATTGACTTGTT (SEQ ID NO: 328)	GGAACACCATCATTCCAACC (S EQ ID NO: 329)	232
34.1924 78	DG13S1926	TACAAGCTCCACCGTCCTTC (SEQ ID NO: 330)	TGAGTTGCTGCCTCTTCAAA (S EQ ID NO: 331)	261
34.2202 27	DG13S1469	TGCTAATGGGCAAGGAATA (SE Q ID NO: 332)	GCTAAATGTCCTCATGAATAGC (SEQ ID NO: 333)	382
34.3014 48	DG13S351	TGTCCTGCAGACAGATGGTC (SE Q ID NO: 334)	CCTCCGGAGTAGCTGGATTA (S EQ ID NO: 335)	294
34.3878 83	DG13S26	GAGACTGGCCCTCATTCTTG (SE Q ID NO: 336)	AAGAAGCCAGAGACAAAGAAA TACA (SEQ ID NO: 337)	330
34.5354 41	DG13S30	CATCTATCTTTGGATTCACTGGT (SEQ ID NO: 338)	TGCTCCCAACATCTTACCAG (S EQ ID NO: 339)	388
34.5655 94	DG13S1435	TGTCCTCTGGTCATTTCTATGGT (SEQ ID NO: 340)	CATGAATGAGAAGTGATGAATG (SEQ ID NO: 341)	235
34.6598 58	DG13S1446	AACACGGGAAATTCCAACAG (SE Q ID NO: 342)	TGAAGAACTGAAATTGCCAGTA (SEQ ID NO: 343)	379
34.7122 60	DG13S356	CAGACACTGTAACTGGCTTCG (SEQ ID NO: 344)	GCCACATTGCTATCAGCGTA (S EQ ID NO: 345)	212
34.7387 56	DG13S357	TGTCATAGGCTTGCGGTATTT (SE Q ID NO: 346)	TTGGTAGGGTCCTTTCCTTT (SE Q ID NO: 347)	202
34.7705 71	DG13S1032	GCCTGCTCACTGTTGTTTGA (SEQ ID NO: 348)	CGGTTATCAGAGACTGGTGGT (SEQ ID NO: 349)	211
34.7996 79	DG13S1557	GGCTTATTTATGTACGGCTA (SE Q ID NO: 350)	GGTTAACTCTACTTAGTCCTG ATGC (SEQ ID NO: 351)	158
34.8829 34	DG13S1925	GAACCTCTGCAGGCACCTCTT (SE Q ID NO: 352)	CCTGAAGCGCTTGACTGAA (S EQ ID NO: 353)	456

-151-

34.9326 90	DG13S1484	TGTTGCGTACTCAGCCATA (SEQ ID NO:354)	GACAGGTGTCAAACGGGTCT(S EQ ID NO: 355)	246
34.9425 47	DG13S360	TTGGCTTCTCGCTCTTTCTT(SEQ ID NO: 356)	AGCCATCAGTCACATGCAAA (SEQ ID NO: 357)	350
34.9989 79	DG13S1522	AGATCTCCAGGGCAGAGGAC(SE Q ID NO: 358)	CCTTCCTCCCTCCTTCTCTC(SE Q ID NO: 359)	355
35.0749 62	DG13S1517	CGTCATTGATCCCAATCATCT(SE Q ID NO: 360)	GGCTGATAGCCTCCCTTGTA (SEQ ID NO:361)	235
35.0749 62	DG13S1521	GAGAGAGAGCAGCTTGCATGT(S EQ ID NO:362)	GGCTGATAGCCTCCCTTGTA(S EQ ID NO:363)	172
35.1268 82	DG13S364	ACCTTTCAAGCTTCCGGTTT(SEQ ID NO: 364)	TTCCATCCGTCCATCTATCC(SE Q ID NO: 365)	172
35.3286 63	DG13S1036	TTAAAGTCACTTGTCTGTGGTCA (SEQ ID NO: 366)	TTTGTAGGAATCAAGTCAAATA ATGTA(SEQ ID NO: 367)	216
35.3353 64	DG13S367	CAAACATCACACTGGGCAAA(SE Q ID NO: 368)	TGCTTTGGAATCTTTCTTGCT(S EQ ID NO: 369)	301
35.3719 57	DG13S1901	CTGCCAGGATGTCAGCATT(SEQ ID NO: 370)	TCCACACTTTCTCATCACCTAA A(SEQ ID NO: 371)	440
35.4202 95	DG13S1037	CTTTCGGAAGCTTGAGCCTA(SE Q ID NO: 372)	CCCAAGACCACTGCCATATT(S EQ ID NO: 373)	269
35.4258 41	DG13S1854	TGACAGGTTTGGGTATATTGGA(S EQ ID NO: 374)	TGCTTAATGTAGTGGCAGCA(S EQ ID NO: 375)	124
35.5060 53	DG13S1038	TCCTGCCTTTGTGAATTCCT(SEQ ID NO: 376)	GTTGAATGAGGTGGGCATTA(S EQ ID NO: 377)	334
35.5472 10	DG13S1039	CCATTTAATCCTCCAGCCATT(SE Q ID NO: 378)	GCTCCACCTTGTTACCCTGA(S EQ ID NO: 379)	167
35.6092 52	DG13S1840	ACAACCCTGGAATCTGGACT(SE Q ID NO: 380)	GAAGGAAAGGAAAGGAAAGAA A(SEQ ID NO: 381)	217
35.6192 86	DG13S369	TGACAAGACTGAAACTTCATCAG (SEQ ID NO: 382)	GATGCTTGCTTTGGGAGGTA(S EQ ID NO: 383)	257
35.6279 11	D13S305	TTGAGGACCTGTCGTTACG (SEQ ID NO: 384)	TTATAGAGCAGTTAAGGCACA (SEQ ID NO: 385)	394
35.6566 59	DG13S375	TGAGGGTGTAAGCCCTTATT(SE Q ID NO: 386)	GGAGTTGTGGCCTCTCTCTCT (SEQ ID NO: 387)	192
35.7603 68	D13S219	AAGCAAATATGCAAAATTGC(SEQ ID NO: 388)	TCCTTCTGTTTCTTGACTTAAC A (SEQ ID NO: 389)	125
35.8258 52	DG13S378	TGCTAAGAGGGCAGATCTCA(SE Q ID NO: 390)	GGCTCATAGCCAATTTCTCC (SEQ ID NO: 391)	324
35.8321 27	DG13S32	CGGCATTCTCAATAACCTCAA (SEQ ID NO: 392)	TCTTTGATGAGGATCAATTAGT GG (SEQ ID NO: 393)	214
35.8729 36	DG13S1549	ACGCACACACACACACAC (SEQ ID NO: 394)	TGCCTCTGTAATCCTGTGTAGC (SEQ ID NO:395)	260
35.9123 21	DG13S1473	GCTCTAAGGTGGGTCCCAATA (SEQ ID NO:396)	GGAATGACAAGATCAGTTTAC C (SEQ ID NO: 397)	163

All references cited herein are incorporated by reference in their entirety. While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made

-152-

therein without departing from the scope of the invention encompassed by the appended claims.

5

-153-

CLAIMS

What is claimed is:

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1. Use of a leukotriene synthesis inhibitor for the manufacture of a medicament for treatment for myocardial infarction or susceptibility to myocardial infarction in an individual.
- 10 2. The use of Claim 1, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for myocardial infarction, an at-risk haplotype in the FLAP gene, a polymorphism in a FLAP nucleic acid, and an at-risk polymorphism in the 5-LO gene promoter.
- 15 3. The use of Claim 1, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated lp(a); obesity; and past or current smoker.
- 20 4. The use of Claim 1, wherein the individual has an elevated inflammatory marker.
- 25 5. The use of Claim 4, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9.
- 30

6. The use of Claim 1, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
7. The use of Claim 1, wherein the individual has increased leukotriene synthesis.
8. The use of Claim 1, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.
9. The use of Claim 1, wherein the individual has atherosclerosis or who requires treatment (*e.g.*, angioplasty, stents, coronary artery bypass graft) to restore blood flow in arteries.
10. The use of Claim 1, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio)-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
11. The use of Claim 1, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-

-155-

phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.

- 5 12. The use of Claim 1, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
13. The use of Claim 1, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
- 10 14. The use of Claim 1, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
15. The use of Claim 1, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
- 15 16. The use of Claim 15, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 20 17. The use of Claim 1, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
18. The use of Claim 17, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
- 25 19. A method of treatment for acute coronary syndrome in an individual, comprising administering leukotriene synthesis inhibitor to the individual, in a therapeutically effective amount.
- 30

20. The method of Claim 19, wherein the acute coronary syndrome is selected from the group consisting of: unstable angina, non-ST-elevation myocardial infarction (NSTEMI) and ST-elevation myocardial infarction (STEMI).
- 5
21. The method of Claim 19, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for myocardial infarction, an at-risk haplotype in the FLAP gene, a polymorphism in a FLAP nucleic acid, and an at-risk polymorphism in the 5-LO gene promoter.
- 10
22. The method of Claim 19, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated lp(a); obesity; and past or current smoker.
- 15
23. The method of Claim 19, wherein the individual has an elevated inflammatory marker.
- 20
24. The method of Claim 23, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9.
- 25
25. The method of Claim 19, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
- 30

-157-

26. The method of Claim 19, wherein the individual has increased leukotriene synthesis.
27. The method of Claim 19, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.
28. The method of Claim 19, wherein the individual has atherosclerosis or who requires treatment (*e.g.*, angioplasty, stents, coronary artery bypass graft) to restore blood flow in arteries.
29. The method of Claim 19, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
30. The method of Claim 19, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4-yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.

-158-

31. The method of Claim 19, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
- 5 32. The method of Claim 19, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
33. The method of Claim 19, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
- 10 34. The method of Claim 19, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
35. The method of Claim 34, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 15 36. The method of Claim 19, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
- 20 37. The method of Claim 36, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
- 25 38. A method of decreasing risk of a subsequent myocardial infarction in an individual who has had at least one myocardial infarction, comprising administering a leukotriene synthesis inhibitor to the individual, in a therapeutically effective amount.
- 30 39. The method of Claim 38, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for

-159-

myocardial infarction, an at-risk haplotype in the FLAP gene, a polymorphism in a FLAP nucleic acid, and an at-risk polymorphism in the 5-LO gene promoter.

- 5 40. The method of Claim 38, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated lp(a); obesity; and past or current smoker.
- 10 41. The method of Claim 38, wherein the individual has an elevated inflammatory marker.
42. The method of Claim 41, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, 15 interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9. 20
43. The method of Claim 38, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
- 25 44. The method of Claim 38, wherein the individual has increased leukotriene synthesis.
45. The method of Claim 38, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.

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46. The method of Claim 38, wherein the individual has atherosclerosis or who requires treatment (e.g., angioplasty, stents, coronary artery bypass graft) to restore blood flow in arteries.
- 5 47. The method of Claim 38, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-10 0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
- 15 48. The method of Claim 38, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.
- 20 49. The method of Claim 38, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
- 25 50. The method of Claim 38, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
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-161-

51. The method of Claim 38, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
- 5 52. The method of Claim 38, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
53. The method of Claim 52, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 10 54. The method of Claim 38, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
- 15 55. The method of Claim 54, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
- 20 56. A method of treatment for atherosclerosis in an individual, comprising administering a leukotriene synthesis inhibitor to the individual, in a therapeutically effective amount.
57. The method of Claim 56, wherein the individual is concurrently treated to restore blood flow in coronary arteries.
- 25 58. The method of Claim 56, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for myocardial infarction, an at-risk haplotype in the FLAP gene, a polymorphism in a FLAP nucleic acid, and an at-risk polymorphism in the 5-LO gene promoter.
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59. The method of Claim 56, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated lp(a); obesity; and past or current smoker.
- 5 60. The method of Claim 56, wherein the individual has an elevated inflammatory marker.
- 10 61. The method of Claim 60, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9.
- 15 62. The method of Claim 56, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
- 20 63. The method of Claim 56, wherein the individual has increased leukotriene synthesis.
- 25 64. The method of Claim 56, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.
- 30 65. The method of Claim 56, wherein the individual requires treatment (e.g., angioplasty, stents, coronary artery bypass graft) to restore blood flow in arteries.

66. The method of Claim 56, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
67. The method of Claim 56, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.
68. The method of Claim 56, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
69. The method of Claim 56, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
70. The method of Claim 56, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.

71. The method of Claim 56, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
- 5 72. The method of Claim 71, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 10 73. The method of Claim 56, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
74. The method of Claim 73, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
- 15 75. A method of reducing leukotriene synthesis in an individual, comprising administering a leukotriene synthesis inhibitor to the individual, in a therapeutically effective amount.
- 20 76. The method of Claim 75, wherein the individual is concurrently treated to restore blood flow in coronary arteries.
- 25 77. The method of Claim 75, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for myocardial infarction, an at-risk haplotype in the FLAP gene, a polymorphism in a FLAP nucleic acid, and an at-risk polymorphism in the 5-LO gene promoter.
- 30 78. The method of Claim 75, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated lp(a); obesity; and past or current smoker.

-165-

79. The method of Claim 75, wherein the individual has an elevated inflammatory marker.
- 5 80. The method of Claim 79, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix
10 metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9.
81. The method of Claim 75, wherein the individual has increased LDL
15 cholesterol and/or decreased HDL cholesterol.
82. The method of Claim 75, wherein the individual has increased leukotriene synthesis.
- 20 83. The method of Claim 75, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.
84. The method of Claim 75, wherein the individual has atherosclerosis or who requires treatment (e.g., angioplasty, stents, coronary artery
25 bypass graft) to restore blood flow in arteries.
85. The method of Claim 75, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-
30 ((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)- 1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-

-166-

5 Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.

- 10 86. The method of Claim 75, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.
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- 20 87. The method of Claim 75, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
88. The method of Claim 75, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
- 25 89. The method of Claim 75, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
90. The method of Claim 75, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.

-167-

91. The method of Claim 90, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 5 92. The method of Claim 75, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
93. The method of Claim 92, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
- 10 94. The method of any one of Claims 1-93, wherein the leukotriene synthesis inhibitor is an agent set forth in the Agent Table.
- 15 95. The method of any one of Claims 1-93, wherein the leukotriene synthesis inhibitor is an agent selected from the group consisting of: a complement of a nucleic acid encoding a member of the leukotriene pathway; a binding agent of a member of the leukotriene pathway; an agent that alters expression of a nucleic acid encoding a member of the leukotriene pathway; an agent that alters posttranslational processing of a member of the leukotriene pathway; an agent that alters activity of a polypeptide member of the leukotriene pathway; an agent that alters activity of a leukotriene; an antibody to a leukotriene; and an agent that alters interaction among two or more members of the leukotriene pathway.
- 20 25 96. The method of any one of Claims 1-93, wherein the leukotriene synthesis inhibitor is an agent selected from the group consisting of: a FLAP nucleic acid binding agent; a 5-lipoxygenase binding agent; a leukotriene synthetase binding agent; a FLAP nucleic acid binding agent; a 5-lipoxygenase nucleic acid binding agent; a leukotriene
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-168-

synthetase nucleic acid binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters FLAP nucleic acid expression; an agent that alters activity of a polypeptide encoded by a FLAP nucleic acid, a 5-lipoxygenase nucleic acid, or a leukotriene synthetase nucleic acid; an agent that alters posttranscriptional processing of a polypeptide encoded by a FLAP nucleic acid, a 5-lipoxygenase nucleic acid or a leukotriene synthetase nucleic acid; an agent that alters interaction of a FLAP nucleic acid with a FLAP nucleic acid binding agent; an agent that alters interaction of a 5-lipoxygenase nucleic acid with a 5-lipoxygenase nucleic acid binding agent; an agent that alters interaction of a leukotriene synthetase nucleic acid with a leukotriene synthetase nucleic acid binding agent; an agent that alters transcription of splicing variants encoded by a FLAP nucleic acid, a 5-lipoxygenase nucleic acid, or a leukotriene synthetase nucleic acid; and ribozymes.

97. A method of assessing an individual for an increased risk of MI, comprising assessing the level of a leukotriene metabolite in the individual, wherein an increased level of leukotriene metabolites is indicative of an increased risk of MI.
98. The method of Claim 97, wherein the leukotriene metabolite is LTE4.
99. The method of Claim 97, wherein the level of the leukotriene metabolite is measured in serum, plasma or urine.
100. A method of assessing an individual for an increased risk of ACS, comprising assessing the levels of leukotriene metabolites in the individual, wherein an increased level of leukotriene metabolites is indicative of an increased risk of ACS.

-169-

101. The method of Claim 100, wherein the leukotriene metabolite is LTE4.
102. The method of Claim 100, wherein the level of the leukotriene metabolite is measured in serum, plasma or urine.
- 5 103. A method of assessing an individual for an increased risk of atherosclerosis, comprising assessing the levels of leukotriene metabolites in the individual, wherein an increased level of leukotriene metabolites is indicative of an increased risk of atherosclerosis.
- 10 104. The method of Claim 103, wherein the leukotriene metabolite is LTE4.
105. The method of Claim 103, wherein the level of the leukotriene metabolite is measured in serum, plasma or urine.
- 15 106. A method of assessing response to treatment with a leukotriene synthesis inhibitor by an individual in a target population, comprising:
- a) assessing the level of a leukotriene in the individual before treatment with a leukotriene synthesis inhibitor;
 - 20 b) assessing the level of the leukotriene in the individual during or after treatment with the leukotriene synthesis inhibitor;
 - c) comparing the level of the leukotriene before treatment with the level of the leukotriene during or after treatment,
- 25 wherein a level of the leukotriene during or after treatment that is significantly lower than the level of the leukotriene before treatment, is indicative of efficacy of treatment with the leukotriene synthesis inhibitor.
- 30 107. The method of Claim 106, wherein the level of the leukotriene in steps (a) and (b) is assessed by measurement of the leukotriene in a sample selected from the group consisting of: serum, plasma and urine.

108. The method of Claim 106, wherein the level of the leukotriene in steps (a) and (b) is assessed by measurement of *ex vivo* production of the leukotriene in a sample from the individual.

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109. A method of assessing response to treatment with a leukotriene synthesis inhibitor, by an individual in a target population, comprising:

- a) assessing the level of an inflammatory marker in the individual before treatment with a leukotriene synthesis inhibitor;
- 10 b) assessing the level of the inflammatory marker in the individual during or after treatment with the leukotriene synthesis inhibitor;
- c) 15 comparing the level of the inflammatory marker before treatment with the level of the inflammatory marker during or after treatment,

wherein a level of the inflammatory marker during or after treatment that is significantly lower than the level of inflammatory marker before treatment, is indicative of efficacy of treatment with the leukotriene synthesis inhibitor.

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110. The method of Claim 109, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite (e.g., cysteinyl leukotriene 1), interleukin-6, tissue necrosis factor-alpha, soluble vascular cell adhesion molecules (sVCAM), soluble 25 intervascular adhesion molecules (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9.

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-171-

- 5 111. A method of treatment for myocardial infarction or susceptibility to myocardial infarction in an individual, comprising administering a leukotriene synthesis inhibitor to the individual in need thereof, in a therapeutically effective amount.
- 10 112. The method of Claim 111, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for myocardial infarction, an at-risk haplotype in the FLAP gene, a polymorphism in a FLAP nucleic acid, and an at-risk polymorphism in the 5-LO gene promoter.
- 15 113. The method of Claim 111, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated lp(a); obesity; and past or current smoker.
- 20 114. The method of Claim 111, wherein the individual has an elevated inflammatory marker.
- 25 115. The method of Claim 114, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9.
- 30 116. The method of Claim 111, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.

-172-

117. The method of Claim 111, wherein the individual has increased leukotriene synthesis.
- 5 118. The method of Claim 111, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.
119. The method of Claim 111, wherein the individual has atherosclerosis or who requires treatment (*e.g.*, angioplasty, stents, coronary artery
10 bypass graft) to restore blood flow in arteries.
120. The method of Claim 111, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-
15 ((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-
20 O-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
121. The method of Claim 111, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-
25 fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide
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-173-

otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.

- 5 122. The method of Claim 111, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
123. The method of Claim 111, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
- 10 124. The method of Claim 111, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
125. The method of Claim 111, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
- 15 126. The method of Claim 125, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 20 127. The method of Claim 111, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
128. The method of Claim 127, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
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1/132

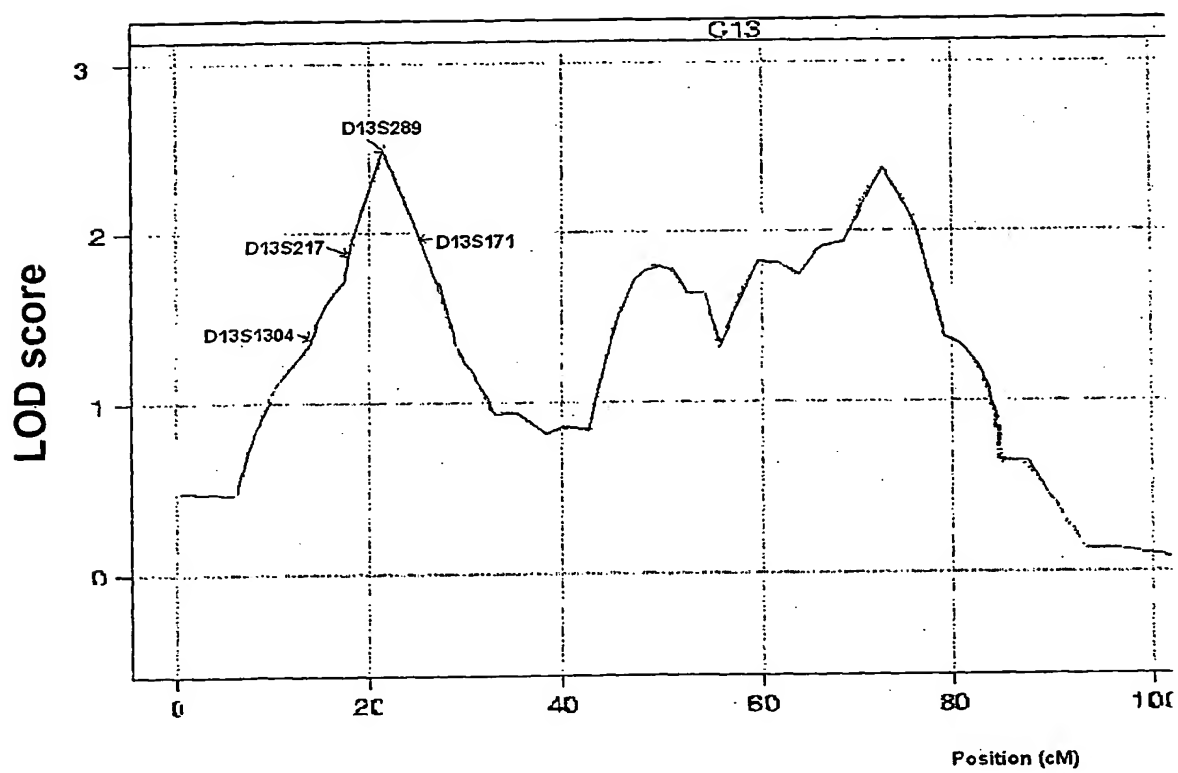


FIG. 1

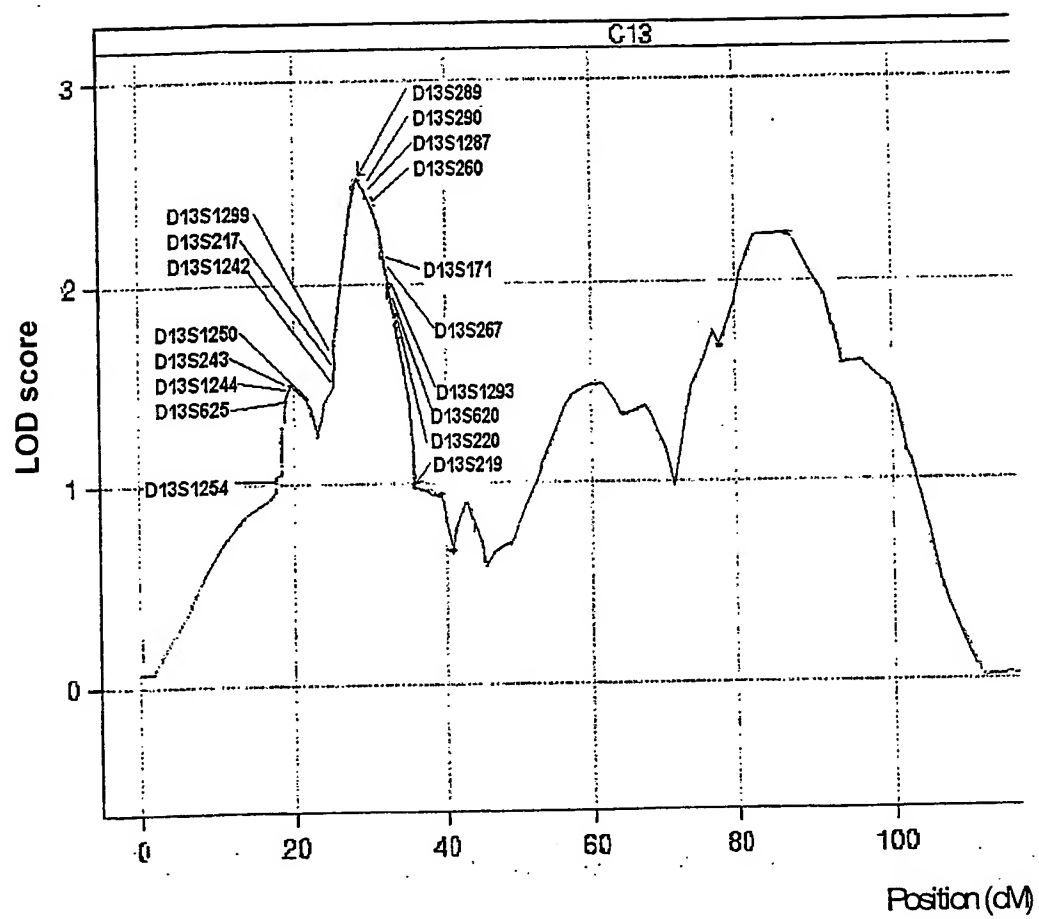


FIG.2

Location of haplotypes showing association
(p value < 10^{-5}) with the disease

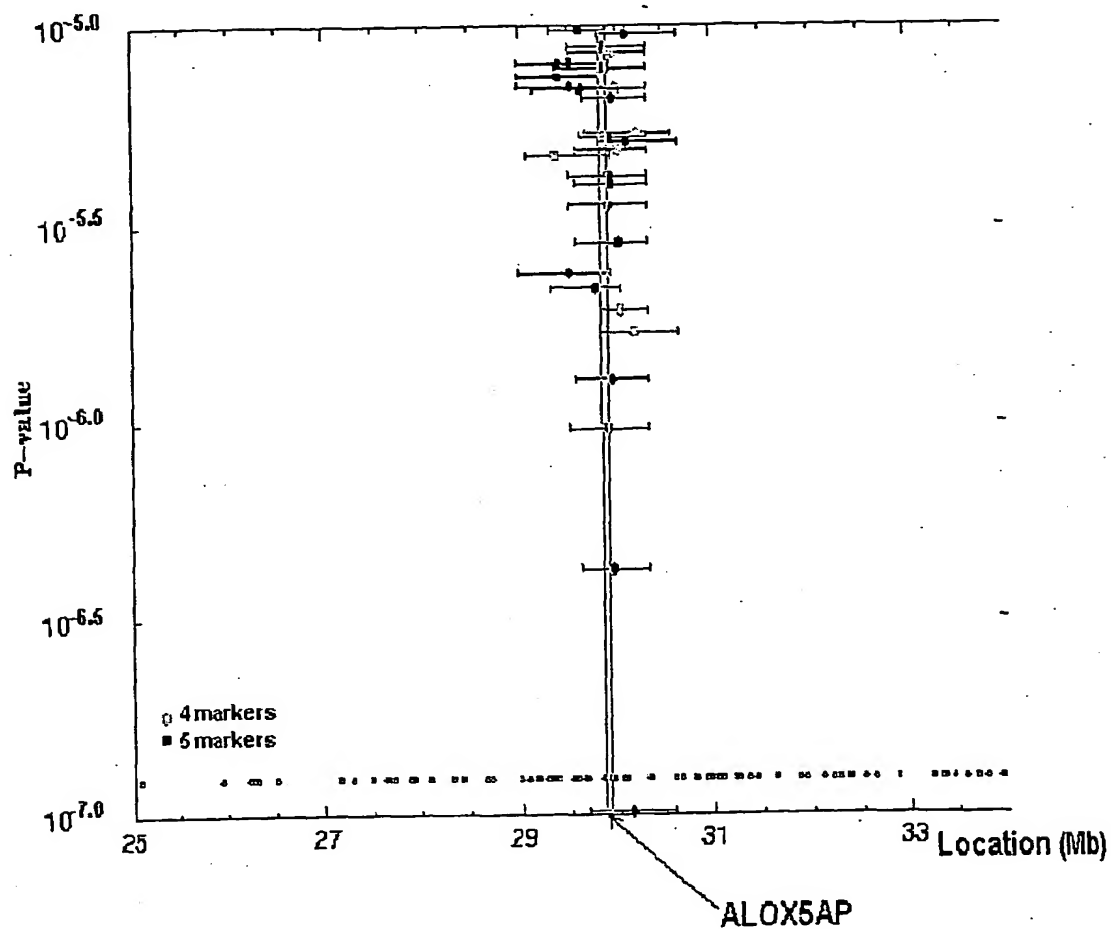


FIG. 3A

Haplotypes showing association
(p value $< 10^{-5}$) with the disease

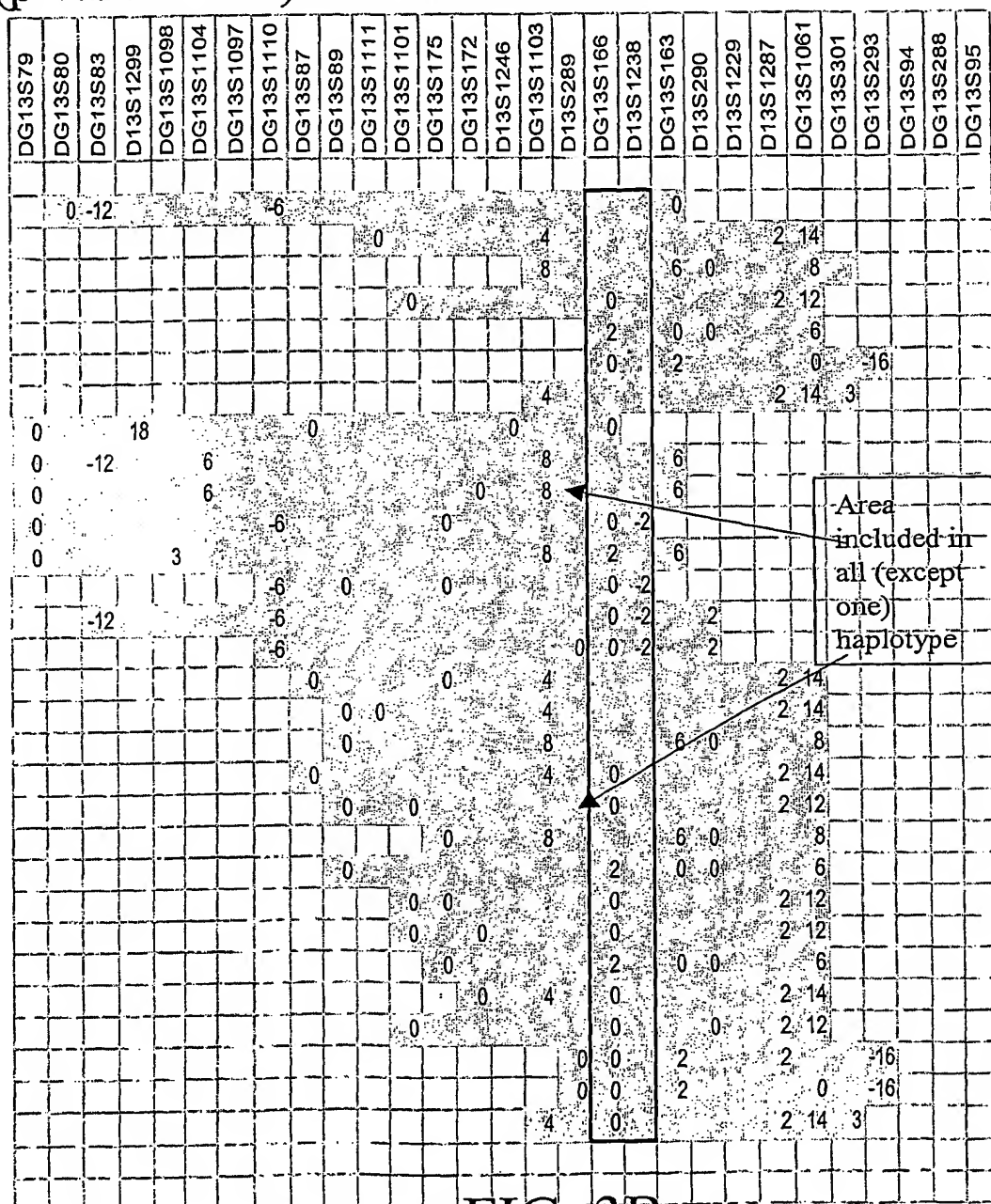


FIG. 3B

Markers and genes around the FLAP gene

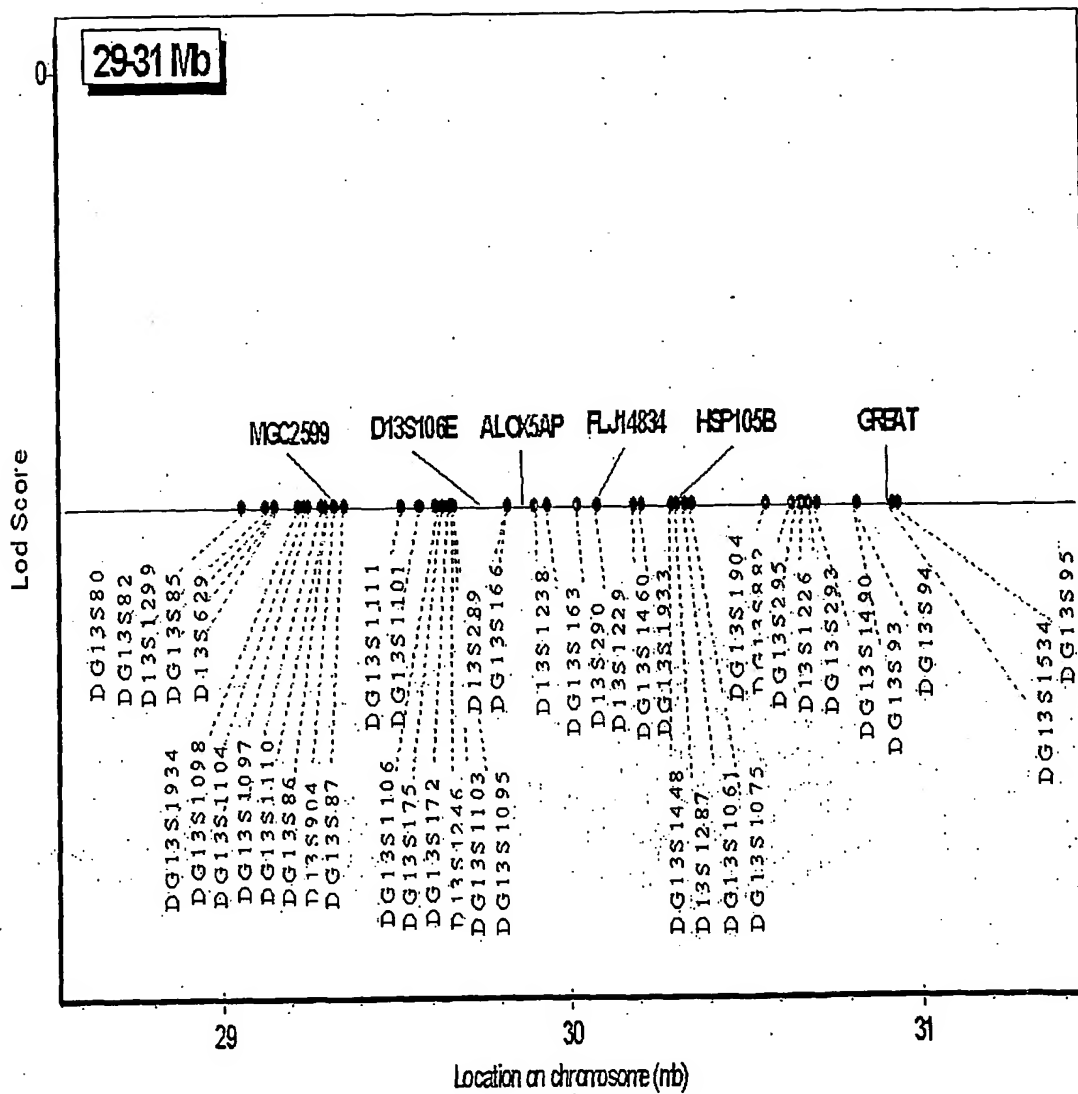
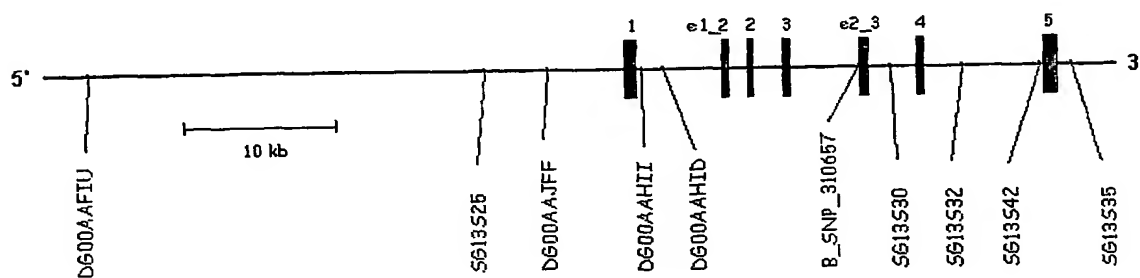


FIG. 4

FIG. 5 Relative location of key SNPs and exons of the ALOX5AP/FLAP gene (exons shown in vertical rectangles). Haplotype length varies between 33 to 68 kb.



7/132

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tacagaccac atgaaaagtg actaaagagc caaaaagctgg ggtggccaga gagaaaatgg 60
aatccagggtt aaaatcctgt tgttttagtca tgtggggttt tttgggttta tgttttttgt 120
ttttgttttt tttgagatgc agtctcactc tgatgccag gctggagtgc agtgacagtgg 180
tgtgatctca gctcactaca acctctgcct ccagagttca agcaattctc ctgcctcagc 240
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aagggtgcatg gactgtccac acagaggccc cttagagcac atttacctcg gtcagtttac 540
cgtggctctg gagctgttc : tcaggctcag acatgtgatt tacttggtta ttatcattat 600
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FIG. 6A

8/132

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ttgaaaaata	ggtcgggcat	ggtggctcac	acctgtaatc	ccagaacttt	gggaggccaa	7740

FIG. 6B

9/132

ggtggggtgga tcacctgagg ccaggaggtc gagaccagcc taaccaatat ggtgaaaccc 7800
 atctctatta aaaatataaa aatgggttggg cgcgggtggct tacacctgta atcccagcac 7860
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 ttaaggtaaa tacttgttga cacatatcta aaatgctgaa ataattattgt ctatttagtgt 11640

FIG. 6C

10/132

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FIG. 6D

11/132

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atgacacaaa	atttacctat	ataacaaacc	tgcattgtgt	tccccgaacc	taaaatgaaa	15840
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tgttatttac	agccattttc	ccaatttttt	tttttaatga	catttccacta	cgttgcccaa	19380
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FIG. 6E

12/132

gattacaggt	gcacacaacc	acacctggct	caattcaaag	agtttttgtt	ttgttctatg	19500
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FIG. 6F

13/132

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FIG. 6G

14/132

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FIG. 6H

15/132

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FIG. 6I

16/132

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FIG. 6J

17/132

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FIG. 6K

18/132

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FIG. 6L

19/132

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FIG. 6M

20/132

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FIG. 6N

21/132

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FIG. 60

22/132

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aagggttttta	aataactgta	cttaagaatc	aactgaccca	ggccagtcct	tactaaaaaa	62220
tcaaaataat	attgattttg	gcagggcgcg	gtggctcacg	cctgtaatcc	cagcactttg	62280
ggaggccgag	gcaggcagat	cacttgaggc	caggtgtctg	agaccagcct	ggccaatgtg	62340

FIG. 6P

23/132

atgaaaccct gtctctacta aaaatactaa aatttagcag tgcattggtg tgcattgctg 62400
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 tctcaaaact atcttaacca

FIG. 6Q

24/132

actattgtaa	ctttctagtt	accctataat	tttactttct	tttttttttt	tccttttttt	66300
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FIG. 6R

25/132

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FIG. 6S

26/132

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FIG. 6T

27/132]

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FIG. 6U

28/132

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FIG. 6V

29/132

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FIG. 6W

30/132

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FIG. 6X

31/132

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FIG. 6Y

32/132

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FIG. 6Z

33/132

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FIG. 6A2

34/132

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FIG. 6B2

35/132

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 aactgagatt ctcatatag gctataatag aaggagcaaa atgtataaag gtagattcta 111900
 gtatacagaa acggtggaaa gaattttcta aggaaaactt agctcctgct tttgatcatt 111960
 caccgaacaa aataatgact gaaaaatata atgggaacag aattggtcta gaagaagaaa 112020
 aactgacagg tgaccgatgt acagtaaatg caagatacaa tggaaagagaa cagtgagaat 112080
 gctctacgga aacatattct agaggacaga aaggccacca cagctcagaa ggtgcagcag 112140
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 attcatgact tgagaatatt ctggagctat aaattttgaa ccactgatgt gcaaaacaag 112260
 acctgaagcc cactccagaa actaaagtga ggcttgctaa ccttctagat tgccctcacg 112320
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 tatacagaat aaacaatgcc tataattatt tttaaaaaga atcatcctaa atttacaaaa 113040

FIG. 6C2

36/132

agacaaaccg	catttccata	atatattgtc	taaatttcag	gaagaaattc	tcaaccccttg	113100
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agaattattc	aaaagaaaaa	ttctattttc	ccaatgggag	aagtgtccaa	aagtttcaaa	113400
gatgtcagaa	aaatcagctt	ttggaagctg	ctgccacaat	tgtcaataag	caggagatac	113460
cagtatgtct	tcaaagagag	aattcattga	aacaagtcac	tgaggctggg	cgtggtggct	113520
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gtcaaaagaa	tgaagtgatg	gaagccagac	tcaaaccaac	tgtgtactct	gtccacacct	116880
cttcagcaat	atggcatatt	gcaaagtagt	gttcagagat	gtgctgttag	taggctgcct	116940

FIG. 6D2

37/132

gctctaacac atgagattaa atttagatag ccacataggg aaatcagttt ttaagaaagc 117000
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 aattaaatta tatatcaact tacttttata ttacagtatt tttgttatac agaagtttat 119940
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FIG. 6E2

38/132

ttagctgggt	gtggtggcag	acacctgtag	ccccagctcc	tcaggaagct	gaggtgggag	120900
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actgcttttg	tggggagcctt	gctatgcaag	ttggtagaaa	aatttatcct	aaagtccag	124440
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tactagtttc	aagaatcagg	caaattgccc	tggtagtagc	actgttcttt	ctgtgggtcac	124560
aagtcaaact	actgtgggtga	ataaaattag	atgatttctt	tagtctttcc	tttttcagcc	124620
cctgtagtca	atttccagtg	ctccattcaa	agaaaaacca	aaaatgtcca	gaatataacc	124680
ttatttttaa	acttgttaac	cactgatttc	acttgttaac	caaatttttt	tttttttttt	124740

FIG. 6F2

39/132

tttgagaatg aatctcactc tgtcaccagg ctggagtgca gtggcatgat cttgggttcac 124800
 tgcaacctcc gectcctggg tactgggttca agcaattctc ctgcctcagt ctcccagata 124860
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 tcggcctccc aaagtgtcgg gattgcaggc atgaaccact gcgcccagcc tgttaaccaa 125040
 atttctaate acacacactt gagggccagt aaatgcctgc tgaaaagagg gtgctgggtg 125100
 tgaggcaact gaggggctaa catactgata gctgctgaaa tcttctacag ctctttcttg 125160
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 gcttgctctt tacccaaatg tagtttagcaa gtccctgggaa ctaaacagca ttgacacact 125280
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 ccataccagc tcatcctccc atttttccag attctgggtc ttctctctta cctagtgtgt 125520
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 gatgtaacct tatttggaaa aatggggcca ggtgcagtgg tgtgcatgtg tagtcccaga 125640
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 aagatcatcc tgatttagga tggaccctaa atccaatgac atttgcctt acaaaagaaa 126000
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 taaccccagc actttgggag gctaaggcgg ggagctcact tgaggtcagg agtttgagac 126360
 caaccaggcc aacctggtga aaccccatct ctattaaaaa taaaaattag ttgggcatgg 126420
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 gcagcaacag tcccttagcc tgcctagaag tctgttaagt catgggcttt ggtaggagga 127380
 agacgagaga aagcagaaca gattattaca aaccagtgct attccccct gatgggtcaa 127440
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 gccaggagtt taagcccagc ctggtcaaca tagcgagacc ttttctctat taaaaataaa 127680
 gaagaaagaa agtaataatg attcaagttc ttaggtattg caaaactgcc ttaatgcata 127740
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 gaagttcatc tccgtgttat accattaaat agataagggc cacactccat agagatgatg 128160
 gtttaagcact ctgtattttc tgggggagtt ctaatttcat gcaattcctt cttcttaaat 128220
 aaaggcaatt ctctaaatat attaccta atacattaggc tttcataatc ttgtaagatt 128280
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 aaaagtcagg ccatgaata agaggtgga agaaaaatct tattctgatt aggaatgcac 128400
 ttaaaagaat aaatttgtga tatatatagt cattttattc tgtattgttt atgtgtgta 128460
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 ttggtgaagac aagaaacaat gtagaaagtt tgacaactta aaaaagta atgtgtgta 128580
 ttggtgaagac aagaaacaat gtagaaagtt tgacaactta aaaaagta atgtgtgta 128640

FIG. 6G2

40/132

gaaagtcctc	ttccaggatt	agcaaaaaaa	tgggtttttt	tttttttttt	tccgagatgg	128700
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tggccaggct	ggtcttgaa	tcctgacctt	gtgatctgcc	cgcccttagc	tcccaaagt	128940
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attaagctgt	agaataaaaa	tctactttta	atagctggca	tagtgccctag	tgggttttgaa	129060
gccacaagca	ggtttacaaa	aaacatttta	atccatctga	atctacagaa	aactaagatt	129120
acctaagcag	aaaatgaaaa	tagttcagga	ttaaggaaga	ttaacaaatg	aagagtatat	129180
gtatttttaga	agtattactt	tatattttta	tagtataata	ataatattta	cgttcctaca	129240
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ggttatttat	tatgaaattt	caaaaattta	gtaaaatatc	taattaggat	tataaccaga	129840
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ttttaataca	tttctgcttt	ctctaattcc	aaagaccact	ctaaagaata	agttatttgt	130140
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gtggaaattc	tttttatgat	gctaactgca	tgctaaccag	actttttaat	ttaatacttg	132240
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ccaaaaatat	aaactccgag	taaaagtatc	tgcatgggtg	gcatatgttt	attattttta	132480
gtgtcagcgt	atacattttc	atgccataaa	gttataaaat	gaaaaaatag	tagcctttta	132540

FIG. 6H2

41/132

tattaagttc atgcttatgt agttagtaaa aacaagaaag caattaacat acaaaccatg 132600
 atgggtggtta aacttgcttc agtttgtgtt ttttaaaatt tgaaagtgaag aaatacagct 132660
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 atactccatt aactgaattc 136620
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 aagtaatgaa gtttgtcagt 136740
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 aggccaaacat tggatttctc 137160
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 ctgectgtac catgaaagag 137400
 gtagaataaa gaattataaa 137460
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 tctgcaactc agcctgggtg 138420
 aggccatata tagccagaa 138480
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 taataatagc aggttctgtt 138840
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 agcctttatt tattatgaca 139380
 ttgttcccca ctgacagaa 139440
 tttttttttt tttttttgtt 139500
 atgttcagaa aactgaattg 139560
 cactcctgtc ttagttgaag 139620
 ctctaattct tcttttcttc 139680
 gcacatatat cctatcttac 139740
 aagaagaaag tctaacctcc 139800
 tctctatata tactctact 139860
 gttcaacgct ttcaaacctc 139920
 ttctctctta tgccctggat 139980
 cttaatgaag cctttcttag 140040
 agcacattgt tcacacagat 140100
 ttgcccattt gaatccaagg 140160

FIG. 6I2

42/132

gcaaggacgg	aatcattctc	atctttgtat	gtcctgggaa	ctagaactgt	actgagaca	136500
taataaacac	ttgatatgtt	tgtaattttt	aaataagtta	atgaacggaa	tygctagaaa	136560
aagtgagaag	aaactctggc	ttactgtata	tcatactgtc	atactaaaaa	tatatactga	136620
agacagaatc	acattatata	atcacttttc	acgctatagg	ccatgatcca	ttatgaaaaa	136680
gaggatagta	aaaaaatcac	agggcacaa	ttttgtttct	gtcacacaca	tgtgtacctg	136740
tatattggac	tggaatgtaa	aacgcatggt	ccattgtaga	acgtgggttt	aaaagaggct	136800
tggaaaacac	tgcataatgg	catttcttag	tttagtaca	tttattattt	tcgtaataac	136860
ctcagctata	atataagtct	accatgaagc	attttgggga	gattaaatga	gatgtgaaaa	136920
gtaaatgtgt	tagatagact	gaattcatat	ctatagcttg	tctgataact	tacaaaacat	136980
ttaaccttac	ccacaagttt	tagtttcttc	actaaagtca	ccctgaggac	agtaatggga	137040
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gaattcacag	gagagcaatt	tacaaaaaaa	aagaaattta	ttgatttata	atgtgagata	137940
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agaattttta	caaacaaatg	agggaaatcag	atccagaaag	tgattcttat	aacttagatt	138600
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ctcttgcttt	gatagaaggc	catcttaacg	aggagggaga	cacctgcagg	caaagtcaga	139140
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tttcatcttt	agtaaccatg	cttctatacc	tggttctcct	tggtcaaagt	ttctttcttc	139260
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cacaaaaatg	ggaagaagtg	atgaaaaatt	acagtccaag	aagaagggtc	atagctgttt	140100
aaatcaattg	gtatatttgt	tatctaata	aacccacagt	aacgacaggt	atttaacaaa	140160
tggttctgct	gaatttgacg	attccatttc	ccttacatcc	catatgcaat	ccatcagcac	140220
cccacatcca	acccatcagt	acatcctgtc	agcattgggt	cccaaatata	acctaataat	140280
aacacatatc	ctactatctc	tgctgctaca	actttagtct	gaaatctcat	aatctcccac	140340

FIG. 6J2

43/132

ttgtactact gtagatgact ctgaatgagt cttcttgctt ccattccaca cagcatccat 140400
 actgatctat tttttttttt aatttttttg agagacgggg tcttgccatg ttgcccaggc 140460
 tggctcttgaa ctccctggctt caaggggatcc tcccacctca acctcccaca gtgataggat 140520
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 gcccttccct tgattaaacc cttcaatgaa ttcacattaa gcaaacacc tggccagggtg 140640
 tgatgggttca tgcctgtaat ctccagcactt tgggagacca agatggggagg atcacttgag 140700
 gccaggagct caacatcagc ttagacaaca tgggtgaaact acatctctac aaaaaatata 140760
 agaattagct gggcatgggtg gtgcacctat agtcccagct actcggggcgg ctgagctggg 140820
 aggatcactt gagccctgga ggtcaaggca gcagtgaact gtgattatgc cactacactt 140880
 cagcctggat gaagtggagc aatccccatc ctttggggagg ccaaggcagg cctcctggat 140940
 gcaagggtggc tcacacctgt accatcctgg ccaacatggt gaaaccccat ctctactaaa 141000
 catgagggtca agagatcgag atgggtggcat gcacctgtag tctcagggtac ttggggaggct 141060
 aatacaaaaa ttagctgggc acccggggagg cgaagggttg agtgagccaa gattgcctgg 141120
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 aaggctcaaa tctttcagcc acaagacctt tttatcttcc ttttaccagg caaacacaat 141600
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 cttagtatgt gcttgttggc tcatcagcac gactagctat gacacattt acttatataa tttcattttc 141900
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 ttaataaaaaa tttgtttatt attttggta accagaattc ttacattgtt ttagcaccca 142020
 tcagcaaaat gaacactttg acaattaaca caattttatc tagcaatatg tatttatcac 142080
 atttaaataa aaaaatgctt cttcttcatt aataaaaaagc aatccaggct ggggtcagtg 142140
 gatagcttct gcaactgaact catagtggaa ggcaggagg gaggatcac ttgataccag 142200
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 ccaatgcatt gctgaaatgt taaatccatt aataaagaaa gtacaggggt 142800
 gttcatgctt gtaatcccag cactttggga ggccaagggt ggcagatcac ttaaggctcag 142860
 gaattcaaga acagcctggc taacacagtg aaaaatgcaa aatacaaaat aagccgggag 142920
 tgggtggcgca tgcctgtaat cccagctact cccgaggctg agggggggaga atcgcttga 142980
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 catctcaaaa aaaaaaagta aaaagtatat agttgattct gcagggactt aaaaaagtat 143100
 aaatatcttt ttttaacatc caaagctctg atatctgcag gtttatgact aactactagc 143160
 tcaactcccat gaatacacgt atgtaaacag gctctataca atctacaatc ccagactaag 143220
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FIG. 6K2

44/132

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tactttgtag	gattattatt	ttttaaacag	ggaccaacaa	taaataaactt	ctctacttga	144480
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taaatcagta	ctgggtgtcaa	agaaatcata	atctcacac	tttataaata	cagcatgtgg	144600
caagggattt	tcccatctta	tatagtaata	aaattttcag	ctgtgccatg	gctaaaaagt	144660
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tgtgagcaaa	gaaatgacaa	gccgttcaat	gctgttagag	aatgaaattc	aagggttccaa	148020
tgatctgaac	ttgtgtcccc	tcaaattcgt	atgttgaaat	cttaatcctc	aatgcaacag	148080
tattaagaat	ttggggcttt	aggaggtaat	ttggttttga	gggtggagcc	ctcatgaata	148140

FIG. 6L2

45/132

ggatgagcac ctgaggtagc ctctttgacc cttccaccat gtgaggacac accacgaagg 148200
 caccatggtg gaagcagaga gtgagcactc ccaagacact gaatctgcca catcttgatt 148260
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FIG. 6M2

46/132

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FIG. 6N2

47/132

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FIG. 602

48/132

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FIG. 6P2

49/132

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ttagctctga	agactcaact	gagcaacttt	caggggttat	ataccctata	ttcagaaaaa	163980
aactactacc	atctctcatt	taccctaaga	attcatagga	gagcatgtct	taaagctgat	164040
caataaccaa	accaaacatt	ttattgatca	tattacattt	ggaaagcaaa	atgaatttcc	164100
taaaattttct	tccctgatta	gcaaaatagt	gcctccgaac	acttgagggg	gaaagttgtt	164160
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gtctactcaa	tgtgaagggtg	acaaggacga	agatctttat	gatgatccat	ttccacttaa	167640

FIG. 6Q2

50/132

tgattagtaa	atatactttac	ttttccttat	gattttctta	gtaacttttt	ttctctaact	167700
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ttgtaataat	acccatttaa	gaatccatgg	tatatatgg	aagtgcaaca	actctagaag	167940
agagtgcag	gagttggaaa	aggaaaagaga	aaacagaatt	taaagcaatc	tgtaaaggac	168000
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FIG. 6R2

51/132

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FIG. 6S2

52/132

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FIG. 6T2

53/132

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FIG. 6U2

54/132

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FIG. 6V2

55/132

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FIG. 6W2

56/132

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gaaataattg	taactttatt	aagactcctt	ataaatttat	ctgttcctat	gacctggcta	194940

FIG. 6X2

57/132

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FIG. 6Y2

58/132

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FIG. 6Z2

59/132

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FIG. 6A3

60/132

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ttgatgccaa agaaaattct aagctgcatt gctgcttaca tgggatacca 210360
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tctgtgttag agtcatactg catgatgact tccaactgtc tgggatacca 210480

```

FIG. 6B3

61/132

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FIG. 6C3

62/132

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FIG. 6D3

63/132

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gctcactgca	acctccactt	cctggttcaa	gcaattctgg	tgccctaagcc	tcccaagtgg	222180
ttgggactat	aggtgtatga	caccatgccc	gactaatttt	tgtatttttt	tgtagagaca	222240

FIG. 6E3

64/132

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gggttttggc atgttggcca ggctgggtctc aaactcctga cctcaagtga tctgcctgcc 222300
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acatttataa attatccagt ctaagatatt ttgtgatagc agcccaagca gaccaaggca 222420
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FIG. 6F3

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gagcctaaaa	atgatcattg	ataacagaaa	atgatctctg	ctctcgcta	gggtaatata	229980
ttcagcttca	aagtgggaag	gcatgttttc	caagggcag	ttttctaagt	ccctgttaatt	230040

FIG. 6G3

66/132

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gtagtgatag caaatatatg cctgcatct tgaaatgtaa gactagggtt gracagtata 230100
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FIG. 6H3

67/132

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FIG. 6I3

68/132

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FIG. 6J3

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FIG. 6K3

70/132

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FIG. 6L3

71/132

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FIG. 6M3

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FIG. 6N3

73/132

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FIG. 603

74/132

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FIG. 6P3

75/132

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FIG. 6Q3

76/132

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FIG. 6R3

77/132

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FIG. 6S3

78/132

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FIG. 6T3

79/132

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FIG. 6U3

80/132

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FIG. 6V3

81/132

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FIG. 6W3

82/132

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FIG. 6X3

83/132

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FIG. 6Y3

84/132

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FIG. 6Z3

85/132

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FIG. 6A4

86/132

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FIG. 6B4

87/132

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FIG. 6C4

88/132

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FIG. 6D4

89/132

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FIG. 6E4

90/132

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FIG. 6F4

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```

FIG. 6G4

92/132

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FIG. 6H4

93/132

gactttcacc agattcttga gcgctttcaa caccactgtc taaacaggct ccgtcagaat 335400
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FIG. 6I4

94/132

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caggtcattg	taagtgtgt	gataaaaaatg	ggtgatgaga	tggagcagaa	aaggggaagg	343080
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FIG. 6J4

95/132

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FIG. 6K4

96/132

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FIG. 6L4

97/132

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FIG. 6M4

98/132

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FIG. 6N4

99/132

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FIG. 604

100/132

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FIG. 6P4

101/132

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FIG. 6Q4

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FIG. 6R4

103/132

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FIG. 6S4

104/132

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FIG. 6T4

105/132

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FIG. 6U4

106/132

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FIG. 6V4

107/132

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FIG. 6W4

108/132

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```

FIG. 6X4

109/132

atttctaaac	aataatttga	ataactagtt	cataataact	catttaaatt	gtctttgccc	397800
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acttgcacag	cagctctttt	gatcatttca	tctttcttgg			398800

FIG. 6Y4

Amino acid sequence of FLAP (>alox5ap_protein translation NM_01629)
MDQETVGNVLLAIVTLISVVQNGFFAHKVEHESRTQN
GRSFQRTGTLA FER VYTANQNCVDA YPTFLAVLWSAGL
LCSQVPAAFA GLMYLFVRQKYFVGYLGERTQSTPGYIFGK
RIILFLFLMSVAGIFNYYLIFFGSDFENYIKTISTTISPLLLIP
(SEQ ID NO: 2)

MRNA of FLAP (NM_001629_mRNA)

Acttccccttctgtacagggcaggtgtgcagctggaggcagagcagtcctctctggggagcctgaagcaaactgga
tcaagaaactgtaggcaatgttgcctgttgccatcgtcaccctcatcagcgtggtccagaatggattcttggccataaag
tgagcacgaaagcaggaccagaatgggaggagctccagaggaccggaacacttgcctttgagcgggtctactg
ccaaccagaactgtgtagatgcgtacccactttctcgtgtgctctggtctgcggggctactttgcagccaagttcctgct
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catgaccgtggcccaaatgtgctattcccatgcatttgtttgtttcttacttatcctgttctctgaagatgtttgtgaccaggt
ttgtgtttcttaaaataaaatgcagagacatgttt (SEQ ID NO: 3)

FIG. 7

111/132

FLA310657 / B_SNP_310657 (R = G/A) (SEQ ID NO: 398)

GGGCTACTTTGCAGCCAAGGTAACCTCAGACTTCCCTTTGTTCAITCTCCTTCTATAAAGTGCATCTCAA
GGAGGTTCAAAGGGCAGGCTTTTTGTTGAAAGGACTTTGCCTGACCTCTGGCTCCCATCTGTGAAGCCC
TGGAGAGGTGAGAGCCCTCGGGAGGCCGTGTTTCAGGCATGCTCTGCACCCGTGCAGAGCGC

R

TGTGATAATGCATTGCTAATGCTTGCTCCCTGGTGGCTGGCTGAGAGCTGCTGTGCTGACAAGGGTGGT
TTAAGGCTAAATGTGACTCAGAATCCTTAAGCAGTGTTAGTTTCAATACAAGGGCATTATAAATGAGAG
TGCTGAGGGATCTATTTTGGGACCGCTGTCACTTGGCTCTTCTGCTAATAAGCTTCCAGTG

FLA302465 (Y = C/T) (SEQ ID NO: 399)

GTTTCTGCTAAATGACAGTTGATGGAGGACATTTAGGGTTGCTTGGAGGTCAAGTCAAGGAGGCATTTA
ACATTCTAGTAAAACAAGGAAGTAACAGGCTCCTGAACATGCCACAATGAACCAGATGCAAACCTTTT
CCCTTGGCAGGATTCTTTGCCATAAAGTGGAGCACGAAAGCAGGACCCAGAATGGGAGGAG

Y

TTCCAGAGGACCGGAACACTTGCCCTTTGAGCGGGTCTACACTGCCAAGTGAGTCCTAACCTTGATGTTG
CTAATAAGTGGGGGCATGGGCAGGGGGGCTCCTTCTAGGAGTGATGACCACCTTAATACCACATGTC
TGTCTGAGCCAAGTTTCTGAGCGCCAGGGAGGTGAGGAAGGTTGGACTTCACCAGAGAGGCT

FLA302524 / B_SNP_302524 (M = C/A) (SEQ ID NO: 400)

GAGGCATTTAATCTAGTAAAACAAGGAAGTAACAGGCTCCTGAACATGCCACAATGAACCAGATG
CAAACCTTTTCCCTTGGCAGGATTCTTTGCCATAAAGTGGAGCACGAAAGCAGGACCCAGAATGGGAG
GAGCTTCCAGAGGACCGGAACACTTGCCCTTTGAGCGGGTCTACACTGCCAAGTGAGTCCTAA

M

CCTGATGTTGCTAATAAGTGGGGGCATGGGCAGGGGGGCTCCTTCTAGGAGTGATGACCACCTTAAT
ACCACATGTCTGTCTGAGCCAAGTTTCTGAGCGCCAGGGAGGTGAGGAAGGTTGGACTTCACCAGAGAG
GCTTTGTGGACACCTTTATCATCTTAGTGAGTGCTAGTGTCAAAACAAAGGGAGTGGGGAT

B_SNP_302560 (R=G/A) (SEQ ID NO: 401)

CAGGCTCCTGAACATGCCACAATGAACCAGATGCAAACCTTTTCCCTTGGCAGGATTCTTTGCCATA
AAGTGGAGCACGAAAGCAGGACCCAGAATGGGAGGAGCTTCCAGAGGACCGGAACACTTGCCCTTTGAGC
GGGTCTACACTGCCAAGTGAGTCCTAACCTTGATGTTGCTAATAAGTGGGGGCATGGGCAGG

R

GGGCTCCTTCTAGGAGTGATGACCACCTTAATACCACATGTCTGTCTGAGCCAAGTTTCTGAGCGCC
AGGGAGGTGAGGAAGGTTGGACTTCACCAGAGAGGCTTTGTGGACACCTTTATCATCTTAGTGAGTG
TAGTGTCAAAACAAAGGGAGTGGGGATATGGGGCACATTGGTGGAGGGAGGTGTGATCTCTG

B_SNP_302617 (Y=C/T) (SEQ ID NO: 402)

CTTTGCCATAAAGTGGAGCACGAAAGCAGGACCCAGAATGGGAGGAGCTTCCAGAGGACCGGAACACT
TGCCCTTTGAGCGGGTCTACACTGCCAAGTGAGTCCTAACCTTGATGTTGCTAATAAGTGGGGGCATGGG
CAGGGGGGCTCCTTCTAGGAGTGATGACCACCTTAATACCACATGTCTGTCTGAGCCAAG

Y

TTCTGAGCGCCAGGGAGGTGAGGAAGGTTGGACTTCACCAGAGAGGCTTTGTGGACACCTTTATCATC
TTAGTGAGTGCTAGTGTCAAAACAAAGGGAGTGGGGATATGGGGCACATTGGTGGAGGGAGGTGTGATC
TCTGCAGCTTCAGAAAGATCTGAAAGAGTCATTTGGTTAGAGAAGTTGACCTATTTCTCTGTG

FLA314500 (S = G/C) (SEQ ID NO: 403)

CTGCTGCGTTTGCTGGACTGATGTACTTGTGTTGAGGCAAAAGTACTTTGTGCGTTACCTAGGAGAGA
GAACGAGAGGTAGGTAACTGGGACTACTAAAGAACTGTGGAGCGATTCTTGATTTTTGAGCAGGAAGA
GTGACAATTCAAAACAGTATTTGACTAGATTACGGCTCCGTAGCATCCCCTTGGGTGGGAG

S

GGGAAGGCTGACTAGGACCTCTGATTCTTTTCCCTGAGCTTTGAAGGCTCTGAAAATACAGCTGGGG
GGACTTGCCAGTTTCTTATTAAGCAATTCCTCCGCATGGTGCTGGCTTTCAAAGGGTGCTTCAGTGC
TGTTTGCTGCACGTGCTTGCAGCCCCACACCTGCACTCCCGCCCTGCAGAGTCTGGCGCT

FLA267479 (R = G/A) (SEQ ID NO: 404)

CTCATGGATTTTGTGTTTCCAAGTGGCAAGATGGCGCTCCACCTTTGGTATCCTATTTTAGTTCCTGGC
AGAAAGAAAGGAACAGGCTAATGGCCCTGATGAGTCTACCCCTTTTAAACAGGAGAAAATTTAAAAAAC
AAAAACCATGAAACCTTTCCAGAGGCAACCAAGATTCATTTATCTTTTATTGACCA

R

FIG. 8A

112/132

AACAGACCACATGGTCACTGGTGGTGGCAATGGAGACTGGGGAGATGAATATTTTAAAGGTGGCATATT
CCAGAAGAACACTGTGCACCTGATTGCATTAATGAACCCATTAATGTGCCAAGGGGAGGTTTACCTATGA
GCATGGGCAAAATTAGAACCCACTCTTGGAGCTGCAGGTGAGCCAATCCCACCTAAACAGTGT

FLA267696 (R = G/A) (SEQ ID NO: 405)
ACTGGTGGTGGCAATGGAGACTGGGGAGATGAATATTTTAAAGGTGGCATATTCCAGAAGAACACTGTG
CACTGATTGCATTAATGAACCCATTAATGTGCCAAGGGGAGGTTTACCTATGAGCATGGGCATAATTAGA
ACCCACTCTTGGAGCTGCAGGTGAGCCAATCCCACCTAAACAGTGTGGATGCTACAAGATGG
R
GAAGTAAATTGATTCTATTCCATACCCCTAACCTCTCTCCAAGATGTATTCTTAAAATAGAAGAGGGGAAG
ACAGAAGAAAACATCCAGAATATATTTTTATTGTCTTTTACTTCTTCAGTGCATTTTATGATCAGTGCTT
CTCAATCTGGCAAGGGGCATGCAGGAGGATGTGAGTTTATCAGGAAAACCTACACAACCCCC

FLA267853 (R = G/A) (SEQ ID NO: 406)
GGTGAGCCAATCCCACCTAAACAGTGTGGATGCTACAAGATGGGGAAGTAAATTGATTCTATTCCATAC
CCTAACCTCTCTCCAAGATGTATTCTTAAAATAGAAGAGGGGAAGACAGAAGAAAACATCCAGAATATAT
TTTTATTGTCTTTTACTTCTTCAGTGCATTTTATGATCAGTGCTTCTCAATCTGGCAAGGGGC
R
TGCAGGAGGATGTGAGTTTTATCAGGAAAACCTACACAACCCCCCAACCACAATGCTACCCCCACTCCTG
TGGACCTTCTTTAAGAGAGACTCACTATTATAGATGGAGTTGATACGATTTTAAAGAGAGGCCATATATT
ATTTGCTTTCTGTCTTGAAAACTTGTGATTTTTCTGTATTGTGCTACTGCCAAAGAGAATA

FLA270742 (Y = C/T) (SEQ ID NO: 407)
TGTTCAGTCTCTCATTTGCTGGGGAGTCTAAACTGGAATAAAACACCCACTATCTCCATCAGGCTTGCAC
TAGAGCCCAGCTCTAGCTGGAGAGAAAGAAGCTAACCCGCACAGACACAGGACTGTAGGCAGGGAGCAT
CCGGGGTATTTGGGTCTGGCTCTGATGTGCCTAAGGCCAATTCTCTCTGGCCATGCTGG
Y
GTGCATGAGCTCACTAATCTTCTTTTTGCTTCCATTTTCTCCAATCCTGACTTAGCAAAGGTTGGGC
AAAAGAGACTCTGTGTGAGTTTCGAGCAAAGCCTGAGATGCTGGATTTTCCAAGATACGAGAAGGGGCTG
GGGCTGGGTGAACCTGGTGGTGGAGGAGGGAAGGATTAATTTCCAAGGAGGGGAAGGGGCC

FLA270830 (R = G/A) (SEQ ID NO: 408)
GAGAGAAAGAAGCTAACCCGCACAGACACAGGACTGTAGGCAGGGAGCATCCGGGGGTATTTGGGTCTCT
GGCTCTGATGTGCCTAAGGCCAATTCTCTCTGGCCATGCTGGCGTGCATGAGCTCACTAATCTTCTCTT
TTTGCCCTTCCATTTTCTCCAATCCTGACTTAGCAAAGGTTGGGCAAAGAGACTCTGTGTGA
R
TTCGAGCAAAGCCTGAGATGCTGGATTTTCCAAGATACGAGAAGGGGCTGGGGGCTGGGTGAACCTGGTG
GTGGAGGAGGGAAGGATTAATTTCCAAGGAGGGGAAGGGGCCAGGACATCAGGCCCGGGGACTTTGA
AGAGAGGGTCTGTGGTAGGAGGTAGATCAAGTGGAGTGACACAAAGGTCAGGAAAGAGGAAG

FLA273407 (W = T/A) (SEQ ID NO: 409)
GCTTTAACTTGTACATGACTATGGCCAAGTTCTGGGGCTCTCCAAGCTTCACTTCTCTGTAAAAAG
GGCAATAATATAATACCTGTCTTATTGGGTTTTGTCCATGTTAGATGAGACATTGGGTACAAAGCACTT
GGTCCCGTGCCTGGCACATTTACTGCACTTAATGTATGATAGTTTTCTTATTATTCTAATAA
W
CAATATGGCTTTGGGAGTATAGTTCTGCCACATTGCAGTGGCCAGAGTGAAGGTGGTGAGTGCTTCTG
GGGCCCTGGGAGTCAAGGTTATCCGCATGCCCTTTCTTGCTTGCTCCTCAGTGTGGCTGCCTCTATGTC
CACACCATGCAGATGCAACAGGTAGTTTGAACCTCTGAGGCCACAGTGGGATGGGGAGGCA

FLA274084 (R = G/A) (SEQ ID NO: 410)
TACCGAATCCAGCATTCAAAGTGATGGAAATATGTATATATAGTAATAGTAAATATCAGCACTTAATG
GCCTGATAAGAATGTCACTGCAATGCTGAGTTTGGACCAACATTTGCCTGCTCCTGCCATTGAGCCCGG
GCTCCCCTCCAGAGCTGAGCTGCTGCAAGGGATCTGAGTAACTAGGGCTGTGTCAGAGTGGC
R
ATGACAGCCACCACATGCTAAGGAAGAGATCCCCAAGGACAAGGAGAATCCCACGTGGAGCTACTTGCT
TCTTTGTGCTGCTTGTTTTTCTTATTTCAACCTTCTAAAACACAATCTCTCAACCTATTGTTAGC
TTGCATTTTTCAATCATGAGCACAGCTTTACCTGGCTCCATGCTTTGATTGACTCTACCTGC

FLA275784 (Y = C/T) (SEQ ID NO: 411)

FIG. 8B

113/132

GAGTGGCTCACAGAACTCAGGGAAACACAGCTACCAGTTTATGCGAAGGACATTTTAAAGGATAAAAG
TAGGCAGATAAAGAGATGCATAGGGCGAGGTGTGGAAAGGTCCCTAGTGCAGGAGCTTCTGTCCATGTG
GAGCGGGGGTGACCAACCTCTCAGTACATGAATGAGTTCTCCTTCACCTGCCTATCAGCCT

Y

TACATGTTTCAGCTCCCCAACCCAGTCCTCTTGGGTTTTTATGGAAGCTTCAAGACACCCACATTCTTTC
CCCAGAGTATAGGGCAAGACCTTCTCTGGGGAGGGTTTTAAGACCCACAGTCAGAAAGGTGGGGTGGGG
TCAAGATTAGAGTCTGCTTGACGGGCAGGTGAAAGGGGTAGGGGGAGTAGGTGAGAAAAA

FLA275952 (R = G/A) (SEQ ID NO: 412)

GAATGAGTTCTCCTTCACCTGCCTATCAGCCTCTACATGTTTCAGCTCCCCAACCCAGTCCTCTTGGGTT
TTTATGGAAGCTTCAAGACACCCACATTCTTCCCCAGAGTATAGGGCAAGACCTTCTCTGGGGAGGGT
TTTAAAGACCCACAGTCAGAAAGGTGGGGTGGGGTCAAGATTAGAGTCTGCTTGACGGGCA

R

GTGAAAGGGGTAGGGGGAGTAGGTGAGAAAAATTCTGTTTATTTTTCTTTTTTTTTTTGAGACGGAGT
TTCACCTCTTGTGCCCAGGGTGGAGTGCAATGGCACAATCTCAGCTCACT 3CAACCTCCGCTCCAGG
TTTAAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCGTGTGCCACCATG

FLA277478 (R = G/A) (SEQ ID NO: 413)

CTGGTATACCTAGAAAACATTCCATAAAAGTTAGTAATTGTTGGTCATGTAATGATGACTCTCTAGGCT
AGGATTTTCAGCTTCATTGTCATGCACATGGTGCACCTCAGGGCGTGACCTCTCTGTCTCAGTAACCT
CATCTGAGGACCGGGATAATCATACCGCTTCAAAGGGATGTCATAAAGATTAAATAATATGT

R

TAAGGCTGCTTGCAATTTAGCTGCATTCAACAAATATTTCTGTATCTTTCTCCTCATTTCTCCTTACTTT
CTTGCTTATTATCTGCTCTAGGTATAGATTTTCAGAGAACTAAGCTTGTTACAATCCTTCATAAAATAAC
CAGGTTGGTTAGGGCATTTCGAAGAGTCAATACTGTTTAGTGACTATTCTCTGTTTAACTA

FLA277678 (M = C/A) (SEQ ID NO: 414)

GTAAGGCTGCTTGCAATTTAGCTGCATTCAACAAATATTTCTGTATCTTTCTCCTCATTTCTCCTTACTTT
TCTTGCTTATTATCTGCTCTAGGTATAGATTTTCAGAGAACTAAGCTTGTTACAATCCTTCATAAAATAA
CCAGGTTGGTTAGGGCATTTCGAAGAGTCAATACTGTTTAGTGACTATTCTCTGTTTAACT

M

TTTTGATTGTCCAGGGTCATCTTTTGCTATGTATAGGTTGTTGGCTTCTTCTAGAGAAGTGAGACGAT
GGACAAGTTCCAAGTGAGTGAGGCGACTGGTCAGGATATTCCGCTGAAAAACTCATGTGAGTTCTAATT
CGTGATTGTAATTCATCAGCCTGAGAACAGTAGGACTGTAGTTCAAATGCTCTGTTCCC

FLA278185 (R = G/A) (SEQ ID NO: 415)

CTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCACATGCCACCAC
GCCCAGATAATTTTCTGATTTTTAGTAGAGACGGGGTTTCCCTTGTTGGCCAGGGTGGTCTTGATCTC
TTGACCTCATGATCCGCCACCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACC

R

CGCCCCGGCTCTAGAGGATAATTTTTAAATGTGCTTTTGCAATTTGGAAAATGTGATTGGCATTTTTTTTC
TAATTTTTCTAATATGATACGCTGTCTGGATGCTATGGATTACTTAAACCTCTGGCTACCTAGAAAGATC
TTTAAGTGGTTCTCAACAAGCTTCATACGCAATGTAAATTGTATTATCTCTCAGGATGTGTG

FLA278492 (R = G/A) (SEQ ID NO: 416)

TTACTTTAAACCCTCTGGCTACCTAGAAAGATCTTTAAGTGGTTCTCAACAAGCTTCATACGCAATGTAA
ATTGTATTATCTCTCAGGATGTGTGAGAACATCTGTTTTTCTTCTAATGCAGTAAACATATAAGGGTCT
CTTGGGATATCTTTTAAATAGACTTAATACAACATTTCAGGAATGATAACAAAATATAATCAC

R

GTTGTAAGGGAATGTGAGCATTTCATATTAATAACATTGGAACCTTATGTTTAAATACAGTGTTAAAGT
TGACAAACATGTAGGAGTCAGAAAATTCAATTAAAATTATCACAGTAATATGAATTTAGCCACATCCTG
TGTTAGTTATGAAATCCATTTAACACCACAAACAGTAATATTTTAGCCAGTTTATTCAAAA

FLA278845 (K = G/T) (SEQ ID NO: 417)

TCCATTTAAACACCACAAACAGTAATATTTTAGCCAGTTTATTCAAAAGGAAAACAGGAACTAAACCAC
TTTCATGCAATATATACTCTGTTAATGTGGTCAGGCTAATTTTCTGCTGGGGGAAGGAACTTAACTTTGA
ATATTTGAATGCCAGTCATTTAATCTGAATATCCTATTTCTTGCATGTTGCAAAATTTTT

K

TCAATAAAAGGCAGAAAAAGAAATCTTCTCCATGCTCATCCCTAAGAGAATGGGTTGTCTGTACCCCT
GAGAGCATTTTATGGAGGGGACAACCACTTTTCTAATTTTCTTCCCACTTCTCTGTGGGCACAAATGC
TCTTTGGTTGAAAGAGTTGTAATTCAGTCCCAAGATGAGGTGTGGTTACTGCATCCCTAACC

FIG. 8C

114/132

FLA280183 (R = G/A) (SEQ ID NO: 418)
ACAACACTTCCTCTGGTAAGATTTTCCTGACATCCTCTATAAAAAAGATTGAGATAGTTGACTACCCA
AAATGTTTCCCATTCATTCCAAGCTCTATTCAAGGCAGTAAAGTGCCCGGCTGACAGATTGCATTCCTC
ATCTTTTCTGAAGCTAGCAATGGCCATGCAACAGCATTCTGGCCAATAAGATAGAAGTCGAA

R

TTGAAGGGTGGGATTTCCAAGAAAGCTCGTTGAAGACATAATTCCTCATTTCACTTCTTACTCTTTCTC
TTTCCTGCTTCCTAAAAATGCGGTGCAGATGGCAGACACTTCAAAGCTGTCTCAGGCAATCAGGTGATGT
TAAGGCAGAAACCAGCTTTATGATGGGTAGAACAGGAAGAAAGAGGCACCTATGTTCTTGT

FLA280923 (M = C/A) (SEQ ID NO: 419)
TCCCTACAAATCTCATGTTGACATTTTATCCCTAATATTGGAGGCAGGGCCTAGTAGGAGGTGTTTTGG
TCATAGTGATAAATGGCTTGGTGCCGTTCTCACAGTAACGAGTGAGTTTTTATTCTAGTGTTTCTGCA
AGAACTGATTGTTAAAGAGCTTGGATCCTTCCACCCCTCTCTACTCTTGCTTCCTCTCTC

M

CACCTTGTAATCTCTACAAGCTCTTCACCTCCCTTCTCTCTTTTGCCATAAGTGGAAGATTTCTGAGGC
CTCACCAGAAGCAGATGTTGGTTCCATGCTTCTTGTACAGCCTGCAGAACCATGAGCCAAATCAACTTC
TTTTCTTTATAATTATCCAGTCTCAGGTATTCTTTATAGCAACACAAATGGACTAAGACAG

FLA283400 (S = G/C) (SEQ ID NO: 420)
TGTCCTGAGTTACAGATCTACACAAAATCACAGAGAGTGTTAATCGTTTAGTCTGATGGTCAGGGAC
TTCCAAGAGACATGATTAGAAAACCTGGTGACAAGGAGTCTGGGGAAGAGGCATATGGATACCTCTGAA
CACACACAAAACATGAGAATATGTATCCCATATGAATGTTAACCAAGAGCAGCCACAACAG

S

AAGAGGATTTTAAATCAGCTGAATAAGATGATTCATTCTGACAGCATCAGCTAGTCTCTTTCCCCAGC
CACTGTTGCCCCAGTGGGCTTACATATATCATGGCCATGGGGGCAGGGCTATGTATGGACACAGCAACAT
GAATTTCCACTCATCAAGGCCAATTTGGCTCCAGCCATTGCTGAGTGCTCAGCCTGCCAAGA

FLA283477 / SG13S25 (R = G/A) (SEQ ID NO: 421)
AGACATGATTAGAAAACCTGGTGACAAGGAGTCTTGGGGAAGAGGCATATGGATACCTCTGAACACACAC
AAAACATGAGAAATATGTATCCCATATGAATGTTAACCAAGAGCAGCCACAACAGAAGAGGATTTTAA
ATCAGCTGAATAAGATGATTCAATCTGACAGCATCAGCTAGTCTCTTTCCCCAGCCACTGTT

R

CCCAGTGGGCTTACATATATCATGGCCATGGGGGCAGGGCTATGTATGGACACAGCAACATGAATTTCC
ACTCATCAAGGCCAATTTGGCTCCAGCCATTGCTGAGTGCTCAGCCTGCCAAGATAGAAATCTACGCCA
ATATGGCACCATTTCCCTGGGCTAGAAAACCAACTGGTGGAAGGTTGATTACATTGGACCATT

FLA284410 (R = G/A) (SEQ ID NO: 422)
CAGGGAATACAATGGTGGTTCCACTAACTGACAGCTGAGTTTGCCATCTCCTCGTGCCAGTGAATACA
CAAGCAAGGAAGGGGGTTCTTTCTCACCTAGGGTGACTGATCCTAATTACCAAGGAGAAATTGGACTG
CCACTTCACAATGAGGGTGAGGAGTATGTACTCTATGTGTCTGTGATTAAATGTCAATAGAAA

R

TGACACCAACCTAGTACACAGAGGACTGATCATGGTCCAGGCCCTTCAGGAATGAAGATTTGAGTCACC
AGGCAAGGAACCTTGGACTCACTGAGGAGGGCATATTCCAAGGAGAATATTTTATCTATGTCCATCTATG
TCCATCTATATTCCATCTGTGTTCCCTTGGAATTCCTATTTCATGAACATGGGGAATTCCAA

FLA284815 (M = C/A) (SEQ ID NO: 423)
AATATAGAATGAGTAGTGGAAGGTAGTTATAAATGTAAGTCAAAAACCAACACAACCAATTTGAGAAATG
AGGAAGGTAATAGTGTGAATATGTCTTCTTTATCTTGATATAAATGTATTTGTGCATATATTAACCAG
TTTATTTATTTATTATTATTTTTTGGAGATGAGCTCTCGCCATGTTGCCAGGCTGGTCTTGA

M

CTCCTGGGCTCAACTGATTCTACCATTTAGTCTCCGAGTAGCTGGGACTACAGGCATGCACCACCATA
CCCAGCTGACCAGTTTTTTCTATTCTCTACTTAATTTCTCTACTATACAACATAATATGTGTTAATG
GTAGTTAACTTTATATCTCAGTATTAAGTCACAAGATATCAAAAAGGGAATGCGACTTAGTT

FLA284903 (Y = C/T) (SEQ ID NO: 424)
ATATGTCTTCTTTATCTTGATATAAATGTATTTGTGCATATATTAACCAGTTTATTTATTTATTATTAT
TTTTTGAGATGAGCTCTCGCCATGTTGCCAGGCTGGTCTTGAACCTCCTGGGCTCAACTGATTCTACCA
TTTAGTCTCTCGAGTAGCTGGGACTACAGGCATGCACCACCATAACCCAGCTGACCAGTTTTT

Y

FIG. 8D

115/132

CCTATTCCTCTACTTAATTTCTCTACTATACAAACATAATATGTGTTAATGGTAGTTAACTTTATATCTC
AGTATTAAGTCACAAGATATCAAAAAGGGAATGCGACTTAGTTACAAGCAGAATGAATATCACTCAAAG
ATGAATAAAGAGAAGAGGGTTAGTGCATTTTCTGTTGGATGAGAGAAAGTTTCATTGTTAGG

FLA290195 (R = G/A) (SEQ ID NO: 425)
TCTTTTGTCTCTGTCTCAGCAGCTCTCTATTAAAGATGAATGGCATTTCCAAAGGCTTCACCTCTGATAA
GTGTTCTCTGTCAGCTGCAGCCAGAATCTTAATGTGCGCGCTGTAATTTAATGGCCGTCTCGGCTATTA
ACACGCTCTTCTCGGGTGAAGTGGACTCCCTCCATCCCCGGGCTCTGCACGTGCTCTGCGC
R
CTGGCTGGGGGTGACTCCAAGGAGCTCAGAGCGGGGTGCCCGGCACCTCTCGCCAGGCGCCTTTCGACC
TTCTAAAGCGCGAATGGCTGGACTTTTCTCCCATGTGTGGGGCCCCAGAAGGTGTGGGGCCCCAGAAGG
TGTGGGGTCCCTGCGTTCCACGGAGCCCCGAAGGTTTCCAGTGATGGTGGGGGCTGACCACG

FLA290553 (S = G/C) (SEQ ID NO: 426)
ACGGAGCCCCGAAGGTTTCCAGTGATGGTGGGGGCTGACCACGTTGGTCCCCGTGGGTGCTGTTTTTCAT
GTGCCGGCAGATTGGGATGAGTTTAAAGACAGAAGCGTGTAGGATAGAGAACTTCTTTAAAACTGG
AAATTTTAATCTGGGGATTATACTATTGGACAGTCAAGTGCAAGAGTGAATACACTTCTCA
S
TCCCTCCTCCCAATTTTATTGCGGGATTAGTCAGTCCCCCTCTGCCACATGATAATTGTGAGAACTA
CCAGGTCTTTCATTCTCTGCCATCTGGTTGACCTCTCCAAGAATGGACACCCGGGCAGCCTGGGCCAA
TGAGGCTGTCCTAAGAGTTTAGATGAGAGAAGTCAGTCTTTGACAGGTGATGGAAGCTGTAA

FLA290570 (Y = C/T) (SEQ ID NO: 427)
TCCAGTGATGGTGGGGGCTGACCACGTTGGTCCCCGTGGGTGCTGTTTTTCATGTGCCGGCAGATTGGGA
TGAGTTTAAAGACAGAAGCGTGTAGGATAGAGAACTTCTTTAAAACTGGAAATTTTAATCTGGGGA
TTATACTATTGGACAGTCAAGTGCAAGAGTGAATACACTTCTCACTCCCTCCTCCCAATTT
Y
TATTTGCGGGATTAGTCAGTCCCCCTCTGCCACATGATAATTGTGAGAACTACCAGGGTCTTTCATTCTC
CTGCCATCTGGTTGACCTCTCCAAGAATGGACACCCGGGCAGCCTGGGCCAATGAGGCTGTCCTAAGAG
TTTAGATGAGAGAAGTCAGTCTTTGACAGGTGATGGAAGCTGTAAATGTAAACTCCACAG

FLA292253 (K = G/T) (SEQ ID NO: 428)
TCTCCACCAGCAGCTTTTCTGAGTCTCCAGCTTGCGAGATGGCAAACCATGAACTTCATGGTGTCCATG
AGCATGTGAACCAATTTCTATTATAAATCTGCAATATATATATATAGAGGAGACTTATTATATATTGGT
TCAGTTTCTCTGGAGAGCCTTGGCTAATATAAAGTCTATACTCTACAAAGTGCCCTAGGTAC
K
CAGGGAGTACCCAAGTGTGTCATGACCAGCCCCGACAGCCCTGGCTGCTGGCTTCCCCGACACAACTCT
GCAGCTGCCTTCATCAGCCTTTCTCTCTCAGCTGAACCGAGGGCATTTGAAGCGGGCTCTGGCACTGT
ACCTATGAGGGAGCAATATCTTCCCTACACTGACCTCTTCCGTGCCGAGATGCAGCCCTCC

FLA292576 (W = T/A) (SEQ ID NO: 429)
GGGCCTCTGGCACTGTACCTATGAGGGAGCAATATCTTCCCCCTACACTGACCTCTTCCGTGCCGAGATG
CAGCCCTCCCTGCTGCCACTAGTTACAGTGGTCCATGTTCCCTTTCAAAGTGAAGTTTGTATAAAAGCA
CCTCTTAACCAATGCCAAATAGCTAAGTCTGGGACAAAGATTGCAGGTATTTTGCATTTTCC
W
TGTAACCTCAGAGGGATTGCCATTACACTGATCTGAGCTGCAGAAATACCAGGCAGCCACCTCACCAC
CCAGCAGGTCCACTCTTATACTTTCTCAGAAAGCACAGCCACTCTACTCTTATTCAGTTGAAAAGAATT
TCCAGGAAGGTGTTTCTGCGATTGCCTCAGAAAAGTCAGTTCCCTTTGGGAATTTCCCTTAG

FLA295036 (R = G/A) (SEQ ID NO: 430)
CATTTTATACTAAATTACACACAACAAAGTTGTAGCTCAGAGAGGGAACAAATGGCTTATTTAGGCCA
CCATTTTCTTGAGCCATTATGATTTACACAGGGCTCCCTTGGCCCTGTAAATTGGCAAGGATTCCATT
ATTCAACCCGCATACATGTACAGAGACCCTGCTCTGGCCCAGATAGTATTCTGGGTACAGGC
R
GATAGAGCAGGAAACAAAACAGCTACAGTGATGGACAGGTCAGCCTGCAGCAATGCCCTGCAGTCTCTGC
AAAGGTAGCTGTATGGGTGGGCAGGTGGCTAGCACTTATTGAGCTCTGGAAGGATCTCCCTCTGGCCT
CTCCCTGACACCCATCAATAAACTGAGGAGCATCGGTGGACAGGGGACCTTGTGCCCCCT

FLA296102 (W = T/A) (SEQ ID NO: 431)

FIG. 8E

116/132

GGAGGGGGGCAAAACATTCAAATAACTCAGGAGATAACACAACCTATTTGTTTTAACTG1GAGTTTTTAG
GCAATCACAAAGATCCAGATGTATGTCCAAGCCTCTCTTTGCAATTCCTAATTAACCTCAATGTTGCAAC
CATAGACCTACCTTACAGAGTTCAAAAAATATGCAAAAACCTGCGCTTTCTTCTCTCCTCAT

W

CCCCAAATGCCATTCTGAACATTTCTGTAGTTAAAAAAGATTTCCATGGTGTACCAGGCACTGT
ACACAGTCTGTGTCCCAAGACAAGGAGGTACAGTTCCACATGCGCCCATGACTGGGTGGGCTCTGCAC
TCTCTCTATACCTTTGAGAGCCTGATTTTCTGTGATTGGGCAGAGCTGGCCACCTGGTGCAA

FLA298098 (R = G/A) (SEQ ID NO: 432)

AATCATCTGACTTTAGAGAGTAGACACTTGCTCCATGCATATTGCCTCCAATTCATTCAAGCACT
CCCTGCTCAAGAAGTTCTTTCTTATGTTGAGCTGAAATCTGCAGCCCTATGCGTTTACCCAGCAGTCC
TGGTGCTGTTCCCTAAATCACTTAGACTGTGCCTGCTCTTCTGTGTTTACAGTGTCTAGCT

R

TAATATCCCCCTCTTCGGCCTAACGTTTCTGAAGTCCCTTGCCACTGGGTCTCCTCTCCTCTTCTCCTGTG
TTCTTTCTAAGAACACCTATGCAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCTGAGATCCGGGCAT
CGACTCTGTTAGAATAATCTACGTATGAGTTATTTTTTTGAGAACTATGTGTCATTGCTGAC

FLA298188 (R = G/A) (SEQ ID NO: 433)

TTATGTTGAGCTGAAATCTGCAGCCCTATGCGTTTTACCCAGCAGTCTGGTGCTGTTCCCTAAATCA
CTTAGACTGTGCCTGCTCTTCTGTGTTTACAGTGTCTAGCTGTAATATCCCCCTCTTCGGCCTAACGTT
TCTGAAGTCCCTTGCCACTGGGTCTCCTCTCCTCTTCTGTGTTCTTTCTAAGAACACCTAT

R

CAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCTGAGATCCGGGCATCGACTCTGTTAGAATAATCTA
CGTATGAGTTATTTTTTTGAGAACTATGTGTCATTGCTGACTCATATTAACCTCTGTGGTTAACTAAAAT
CTCAAGATCTCTTTATGTTTGTGAGAACTTATTTAACTTCTCTGGCCCTCCGTTTCTCTT

FLA298230 (Y = C/T) (SEQ ID NO: 434)

CAGTCCTGGTGCTGTTCCCTAAATCACTTAGACTGTGCCTGCTCTTTCTGTGTTTACAGTGTCTAGCTG
TAATATCCCCCTCTTCGGCCTAACGTTTCTGAAGTCCCTTGCCACTGGGTCTCCTCTCCTCTTCTCTGTG
TTCTTTCTAAGAACACCTATGCAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCTCTGAGATC

Y

GGGCATCGACTCTGTTAGAATAATCTACGTATGAGTTATTTTTTTGAGAACTATGTGTCATTGCTGACT
CATATTAACCTCTGTGGTTAACTAAAATCTCAAGATCTCTTTATGTTTGTGAGAACTTATTTAACTTC
TCTGGCCCTCCGTTTCTTCACTGAGCAGTGGAGTGATTGATAACCTCCACCTGTGGTTGCT

FLA298379 (M = C/A) (SEQ ID NO: 435)

AACACCTATGCAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCTCTGAGATCCGGGCATCGACTCTGTGA
GAATAATCTACGTATGAGTTATTTTTTTGAGAACTATGTGTCATTGCTGACTCATATTAACCTCTGTGGT
TAACTAAAATCTCAAGATCTCTTATGTTTGTGAGAACTTATTTAACTTCTCTGGCCCTC

M

GTTTCTTCACTGAGCAGTGGAGTGATTGATAACCTCCACCTGTGGTTGCTGAAGGTCTTGACACAAGAT
GATATAGTTAAAGTAGCTAGCAGTGCCACGTACGGCGGATGCCTCACAACGGTTTGACGCCATCTCTC
TATCTGTGTCTTTGTCTCTCTCTCACACTGGTTTTGGCTTACTGTTAGCAGCTAGCCGAGAT

FLA298507 (M = C/A) (SEQ ID NO: 436)

ACTCTGTGGTTAACTAAAATCTCAAGATCTCTTATGTTTGTGAGAACTTATTTAACTTCTCTGGCC
CTCCGTTTCTTCACTGAGCAGTGGAGTGATTGATAACCTCCACCTGTGGTTGCTGAAGGTCTTGACACA
AGATGATATAGTTAAAGTAGCTAGCAGTGCCACGTACGGCGGATGCCTCACAACGGTTTGC

M

GCCATCTCTCTATCTGTGTCTTTGTCTCTCTCACACTGGTTTTGGCTTACTGTTAGCAGCTAGCCGA
GATAAGTGTGTTTATGGTCTTTGCATGTATTGTTTCTGTAGCATACTGGAGGATTACAAGAGGTGGGG
AGTGAGGGGGCGGTGAGGAGTAGACAAAGGCAGCCAACTCTTCCAAGTTTAGCTTAGAAGGA

FLA298604 (Y = C/T) (SEQ ID NO: 437)

GATTGATAACCTCCACCTGTGGTTGCTGAAGGTCTTGACACAAGATGATATAGTTAAAGTAGCTAGCAGT
GCCACGTACGCGGATGCCTCACAACGGTTTGACGCCATCTCTCTATCTGTGTCTTTGTCTCTCTCTC
ACACTGGTTTTGGCTTACTGTTAGCAGCTAGCCGAGATAAGTGTGTTTATGGTCTTTGCATG

Y

ATTGTTTTCTGTAGCATACTGGAGGATTACAAGAGGTGGGGAGTGAGGGGGCGGTGAGGAGTAGACAAA
GGCAGCCAACTCTTCCAAGTTTAGCTTAGAAGGAAGGAGCGGTAAACCCTAGTTGAATGTTGGACTGAA
GCAGGTTTTGTTTTGTTTTGTTTAAAGGATAGGGAAGATCTGTGCGTGTTTCCAGGATAAAG

FIG. 8F

117/132

FLA298987 (Y = C/T) (SEQ ID NO: 438)
CGTGTTCAGGATAAAGAAAAGGAGAGAATATGATATTAAAGATTCTGGAAGTGGGAGAAGGAGCAAT
GAAATACAGACTTGAAGTCAGTGGCATGGACAGGGTCAAGATCACAGTTAGAGGATGCAGCCTTAGAGA
AAAGGAAGGGGCTCGGTTCTCTGAGCAAGGAGGGAAGAAGAGAGGCAGATGCAGAGAAGTA

Y
GGCACATCGTGCTGCTGGTTGTAGAAATAACCTCTGACTTTTAATAAAGTCATCCCTCGGTATCCCTGG
GGGATTAGTTCTATGACCTCCCTCGGATGCCAAAATTCGTGGATGCTCAAGTCCCTGATATAAAATGGC
ATAGTATTTGCATTTAACCTACACACATCCTCCATATCCTTTTTTTTTTTTTTTTTTTTTTTTT

FLA299063 (R = G/A) (SEQ ID NO: 439)
AGACTTGAAGTCAGTGGCATGGACAGGGTCAAGATCACAGTTAGAGGATGCAGCCTTAGAGAAAAGGAA
GGGGCTCGGTTCTCTGAGCAAGGAGGGAAGAAGAGAGGCAGATGCAGAGAAGTACGGCACATCGTGCT
GCTGGTTGTAGAAATAACCTCTGACTTTTAATAAAGTCATCCCTCGGTATCCCTGGGGGATT

R
GTTCTATGACCTCCCTCGGATGCCAAAATTCGTGGATGCTCAAGTCCCTGATATAAAATGGCATAGTAT
TTGCATTTAACCTACACACATCCTCCATATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGT
GAGATGGAGTCTTGCTCTGTCGCCCTGGCTGGAGTACAGTGGCTCGATCTTGGCTCACTGCA

FLA299772 (S = G/C) (SEQ ID NO: 440)
CTCAGCCTCCTGTGTAGCTAGGATTACAGGCCCCCTCCCCACCCCCACCCCCAACAACTGGCTAATTTT
TGTATTTTGTAGATAGAGATGGGGTGTCAACACGTTGGCCTGGCTGGTCTTGAACCTCCTGACCTCAGGTGA
TCTACCCGCTTCAGCCTCCCAAAGTGATGGGATTATAGGCATGAGCCACTGTGTGTGGCCTA

S
ATTACTTATAATACCTGATAGAATGTAAATGCTATGTAAACAGTTGTTATACTGTATTGTTAAAAGACA
GTAACAAGAAAAAAATCTGTACATGTTAGTCCAGACAAATGGTTTCTGTTTTTTTTTTTTTTTTTTTT
AATATTTTTGGTCAGTGGTTGGTTGACTCCAGGAATGCAGAACCCGAGATATAGAAGGTTG

FLA299843 (Y = C/T) (SEQ ID NO: 441)
TATTTTTAGTAGAGATGGGGTGTCAACACGTTGGCCTGGTCTTGAACCTCCTGACCTCAGGTGATC
TACCCGCTTCAGCCTCCCAAAGTGATGGGATTATAGGCATGAGCCACTGTGTGTGGCCTAGATTACTTA
TAATACCTGATAGAATGTAAATGCTATGTAAACAGTTGTTATACTGTATTGTTAAAAGACAG

Y
AACAAGAAAAAAATCTGTACATGTTAGTCCAGACAAATGGTTTTCTGTTTTTTTTTTTTTTTTTTAA
TATTTTTGGTCAGTGGTTGGTTGACTCCAGGAATGCAGAACCCGAGATATAGAAGGTTGATTATGCGT
TCAGAGGCAGGAATACCATCTTGGGTTCCAGAAAGAAAATGATCAGCATTCTTCTGTCATAC

FLA299980 (R = G/A) (SEQ ID NO: 442)
ATAATACCTGATAGAATGTAAATGCTATGTAAACAGTTGTTATACTGTATTGTTAAAAGACAGTAACAA
GAAAAAAATCTGTACATGTTAGTCCAGACAAATGGTTTTCTGTTTTTTTTTTTTTTTTTTAATATTT
TTGGTCAGTGGTTGGTTGACTCCAGGAATGCAGAACCCGAGATATAGAAGGTTGATTATGC

R
TTCAGAGGCAGGGAATACCATCTTGGGTTCCAGAAAGAAAATGATCAGCATTCTTCTGTCTACTCTGGT
AAAAACAGATCTTTTGAATGGACAGGTGTATTAAACCTGTGGAGCTGGCTGGGCTGGCGGCTCACGC
CTGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGATCACGAGGTCAGGAGTTCGAGACC

FLA300662 (R = G/A) (SEQ ID NO: 443)
TATGCCCCGAGAGTTTGAAGTCCCGGCTGCACCTCTCCCCAGCAGCAGGTTGACTCTGGAAAGTTGCA
GCGTTCTTACCTACAGAGTGGGAACAGTACTACCCATTGCACAGAGTGGGTGCAAAGCTCTGTGACGGA
ATACATGGCAAGTGCCACCACATTGCCTGGGATGAGGTGGGCCCTTCCTTTACGTAAGAGA

R
CCCTACAGATACACTCAAAGTGGGCACATTCTTACAGAAGGAGTGTTATTTGTGTAGAAAAGAAAAACA
TGAAAGGCTTTTATTCCTATACACAATAAAGCACCCCTTTAATGTCCTTTTGGAGGAGGATAATATGAAA
TTGATGAAAAGGAACCCGTGTTGGATCCCTGACAATCACATGTATCCCTTTTTTCACTCT

FLA300864 (R = G/A) (SEQ ID NO: 444)
CCTACAGATACACTCAAAGTGGGCACATTCTTACAGAAGGAGTGTTATTTGTGTAGAAAAGAAAAACAT
GAAAGGCTTTTATTCCTATACACAATAAAGCACCCCTTTAATGTCCTTTTGGAGGAGGATAATATGAAAT
TGATGAAAAGGAACCCGTGTTGGATCCCTGACAATCACATGTATCCCTTTTTTCACTCTT

R
AAAAAGGAGTAAAGGAATAAATAAGAAGGGGAGAGGGGGCAGAGAGACCTTCACCGCCCCCCCCCACC
CCCCATCATCCAATCTATAGTCAAACCCCTCCAGACTGTGTCTCTTGGCATCTCTGACACCCCCCACC
CACCACCCAGTCAATTCCTATCTTATCCCCCTATCCTGGATCTGATTCTGCTAAGTTCTCTG

FIG. 8G

118/132

FLA302094 (R = G/A) (SEQ ID NO: 445)

GAACATTCTGAACCACAGACAGTTCTTTACCCTGAACCTTTGCATATTTTGTCTCTTAGCTTAGAGCG
GCCCCCTCTCCCTCCGTCTGCTTGGCTAATTTCTACTTGTCTTTCAGATTTTATCTTAGATGTCATTCCC
TCAAGGAATCCTTCTGTGACTCAACATGGAATTAAGTTGCCTCCTTTGACCCTGAAAGCACC

R

TGTACTCAATCTCATCTTGGCATGACTCACTTTGCTGTGTGGAATGTCTGCTTTCCTTGTGTTGTCTATT
CCTTTAGACTGTAAGATCCTAGAAAGTGGGGGCCGTGCCTTGCTCATGACTGTGTTTCTAACACCAAAC
ACAGTGTTCAGTAGAGAGCAGCTGCTGAGTACGTTTCTGCTAAATGACAGTTGATGGAGGAC

FLA303769 (W = T/A) (SEQ ID NO: 446)

TCATCTAGGTATTTTAAATTGTTTCAGTGAGGTGTAGGCATGAGGGGATTGGAGGGGGCATCTCCTCCA
TTGCAGTTTTTTCATTGGCTGCTTTGCTCCCTCAGCTCCGAAATCGCTGGGCCACTCTCGAACGCATTAG
TACGGTAGTCACAGGTTGATTGCCTGGCCCCCTTGCCCTCTGTGGGCATTTTCCCTTTCAGAC

W

GCCCCGTGAGTACTCACAGTGCTGCTACAGTGGGCCACCTAGATCTCCCTCTTCTCCATGCTCCACGT
GCTCTGGGCTCCACTCCCTTCTCCCAAGCACTTCTGTCCAGGGCTATTCCAGCAGTCTGACCTCAAGGA
AATCCTTTGCTAAACTGATTATAGAGAGGTTTCTATTTTAAACATTTAGGTCTTCCATGTATT

FLA303796 (Y = C/T) (SEQ ID NO: 447)

TGAGGTGTAGGCATGAGGGGATTGGAGGGGGCATCTCCTCCATTGCAGTTTTTTCATTGGCTGCTTTGCT
CCCTCAGCTCCGAAATCGCTGGGCCACTCTCGAACGCATTAGTACGGTAGTCACAGGTTGATTGCCTGG
CCCTTGCCCTCTGTGGGCATTTTCCCTTTCAGACAGCCCCCTGAGTACTCACAGTGCTGCTA

Y

AGTGGGCCACCTAGATCTCCCTCTTCTCCATGCTCCACGTGCTCTGGGCTCCACTCCCTTCTCCCAA
GCACTTCTGTCCAGGGCTATTCCAGCAGTCTGACCTCAAGGAAATCCTTTGCTAAACTGATTATAGAGA
GGTTTCTATTTTAAACATTTAGGTCTTCCATGTATTAATTCTCAGAATCAATTTAAGATGTTT

FLA303957 (Y = C/T) (SEQ ID NO: 448)

TCCCTTTCAGACAGCCCCCTGAGTACTCACAGTGCTGCTACAGTGGGCCACCTAGATCTCCCTCTTTCTC
CATGCTCCACGTGCTCTGGGCTCCACTCCCTTCTCCCAAGCACTTCTGTCCAGGGCTATTCCAGCAGT
CTGACCTCAAGGAAATCCTTTGCTAAACTGATTATAGAGAGGTTTCTATTTTAAACATTTAGG

Y

CTTCCATGTATTAATTCTCAGAATCAATTTAAGATGTTTAAAGGTGTGATTAAAGACATTTTAAACCA
TTTGGAGGAGAGTACAGAAATTATGTCACCTTGCTGTGACGCTCTTTGCACCATCTGCAGAGAAAGATA
TAGAGTCCCGCTTGGACACATCCACATGCAAGAGGTGCAAGAAGGTGTCTTTGATGAGGC

FLA303967 (W = T/A) (SEQ ID NO: 449)

ACAGCCCCGTGAGTACTCACAGTGCTGCTACAGTGGGCCACCTAGATCTCCCTCTTTCTCCATGCTCCCA
CGTGCTCTGGGCTCCACTCCCTTCTCCCAAGCACTTCTGTCCAGGGCTATTCCAGCAGTCTGACCTCAA
GGAAATCCTTTGCTAAACTGATTATAGAGAGGTTTCTATTTTAAACATTTAGGTCTTCCATGT

W

TTAATTCTCAGAATCAATTTAAGATGTTTAAAGGTGTGATTAAAGACATTTTAAACCATTTGGAGGAG
AGTACAGAAATTATGTCACCTTGCTGTGACGCTCTTTGCACCATCTGCAGAGAAAGATACTAGAGTCCCG
CCTTGGACACATCCACATGCAAGAGGTGCAAGAAGGTGTCTTTGATGAGGCAAGGTCAAAA

FLA304170 (Y = C/T) (SEQ ID NO: 450)

ATTCTCAGAATCAATTTAAGATGTTTAAAGGTGTGATTAAAGACATTTTAAACCATTTGGAGGAGAGT
ACAGAAATTATGTCACCTTGCTGTGACGCTCTTTGCACCATCTGCAGAGAAAGATACTAGAGTCCCGCCT
TGGACACATCCACATGCAAGAGGTGCAAGAAGGTGTCTTTGATGAGGCAAGGTCAAAACTT

Y

CTCCCCAGACGAAATCCAAAGAAAGCATTCCCTACTATGCTATATCAGTTTGGAAAGAAAACTTCTGCC
AGGTGACTGCATTCTCACTGGTCACTTGTGTTCCCTATGGACTCCTCAGCTCAACCAATTTGGAGAAGT
TATGGTGCAATTTACCATATCTGGTTAGAAGTTAAGTTTCCAATTTGCTGGCAATGAAGAA

FLA304334 (Y = C/T) (SEQ ID NO: 451)

CAAAGAAGGTGTCTTTGATGAGGCAAGGTCAAACTTCTCCCCAGACGAAATCCAAAGAAAGCATTCCCT
ACTATGCTATATCAGTTTGGAAAGAAAACTTCTGCCAGGTGACTGCATTCTCACTGGTCACTATTGTGT
TCCTATGGACTCCTCAGCTCAACCAATTTGGAGAAGTTATGGTGCAATTTACCATATCTGG

Y

FIG. 8H

119/132

TAGAAGTTAAGTTTCCAATTTGCTGGCAATGAAGAAGAAATGGAGCAGGCCAGGCTGTGTAGTTTCTGC
CACGTGCCCCCGGGAGTGAACAGCTCTGTTTGTAAAGAAGCCATGGTGCTTAGACCTGGGCTCGCTAGTT
GCCAGCCTCCAAATTGCAGAAAGTGCCTTTGGTTGGTGGCTATGCTGTGTCACTTGGGAAGG

FLA304512 (Y = C/T) (SEQ ID NO: 452)
GGTGCATTTTACCATACTCTGGTTAGAAGTTAAGTTTCCAATTTGCTGGCAATGAAGAAGAAATGGAGC
AGGCCAGGCTGTGTAGTTTCTGCCACGTGCCCCCGGGAGTGAACAGCTCTGTTTGTAAAGAAGCCATGGT
GCTTAGACCTGGGCTCGCTAGTTGCCAGCCTCCAAATTGCAGAAAGTGCCTTTGGTTGGTGG

Y

TATGCTGTGTCACTTGGGAAGGTCGTTTGGAAAGTTCCACAGTCGTTGTGGGGTGGCCAGAGATTAAAAAG
CGTAAGAGGAGAGTGGAAAGTGATTGTTGCTGCTTGGGCATCCCCACCGTGTGGGTGCTGCAGCCCAGC
TCTCAAACCCATGGGTCTGTACACTCAACCTCCATGAGAGGGAAGGAGAAGGATGAGGGAG

FLA304583 (R = G/A) (SEQ ID NO: 453)
GCCAGGCTGTGTAGTTTCTGCCACGTGCCCCCGGGAGTGAACAGCTCTGTTTGTAAAGAAGCCATGGTGC
TTAGACCTGGGCTCGCTAGTTGCCAGCCTCCAAATTGCAGAAAGTGCCTTTGGTTGGTGGCTATGCTGT
GTCACTTGGGAAGGTCGTTTGGAAAGTTCCACAGTCGTTGTGGGGTGGCCAGAGATTAAAAAGC

R

TAAGAGGAGAGTGGAAAGTGATTGTTGCTGCTTGGGCATCCCCACCGTGTGGGTGCTGCAGCCCAGCTC
TCAAACCCATGGGTCTGTACACTCAACCTCCATGAGAGGGAAGGAGAAGGATGAGGGAGGGGAGAGAT
AGCCATGGAAAGGTAGGAACTAAGCAGGCAGGGTGGAGAGTTTCTGTAAGACAAAACTGT

FLA305089 (R = G/A) (SEQ ID NO: 454)
GGCAGCTACATGCTGGCAAAAGCCAGAGGCAGCTGGTCTGTTTGCCTGTGCCAGGAAACCACTGGGAAT
GGGGTTGTGTGTTATTCTAGGAGAAAGTCGTCCAGCAGCAGCTTCTCCAGGGGCATCCAAGAGCACTG
AAAAGGGTTGCAAGATGACCCATGAGGCTGCAGGAAGAAAAGAACATGCATTTAATCTTGCT

R

TCTGAAAAGTAAGACATGAAGCTTTCCTCATTTTTAATATACACATGGACAGTAGTATGTGTATATAGT
TTATATGCAAATATACTTGTATAAGGTTGCATGCTCAAATTTTGGTTTCATGGGGTGTGGGATCATA
AATGTTTAGGGACCATGGCTATCAAGGAAAAACAGCATGAAGGATAAATGATACTGGTGGAT

FLA305505 (W = T/A) (SEQ ID NO: 455)
ATGTATTTTATAGCATAAAACACAACCTGCTGACTGATACAGATAGCTCAAGATTCTGGGGCAGCTGCTGA
ACAGATACACTAGCCAGTGTGGCTCATCGGCTCAGACTTGGCCTTAATTAATGGGCTGTCCCTCCACCC
ATCTCCCATGAGGGCAGAGCTGAGCCAGGGTTTGGAGAGCTAAAAGGAATTGGACCTGGACTC

W

GTTACAGTGTATATTTTAATTCTAATTAATTATTCTTTTGAAGACAGAGTCACACTCTGTTGCCTAG
GCTGGAGTGCAGTGGCAGCATCTTGGCTCACTGCAACCTCGGCCTCCAGGTTCAAGTTATTCTCCTGC
TTCAGCCTCCTGAGTAGCTGGGATTATAGGCACATGCCCCCATGCCTGACTAATTTTGTAT

FLA305678 (Y = C/T) (SEQ ID NO: 456)
GAGCTAAAAGGAATTGGACCTGGACTCTGTTACAGTGTATATTTTAATTCTAATTAATTATTCTTTTG
AAAGACAGAGTCACACTCTGTTGCCTAGGCTGGAGTGCAGTGGCAGCATCTTGGCTCACTGCAACCTCG
GCCTCCAGGTTCAAGTTATTCTCTGCTTCAGCCTCCTGAGTAGCTGGGATTATAGGCACA

Y

GCCCCCATGCCTGACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTACCATGTCAGGCTGGTCTTGA
ACTCCTGACCTCAGGTTATCCACCCGCCTTGGCCCCCTCAAAGTGTGGAATTACAGGTGTGAGCCACCG
TGCTTGGCCTGTTTACATGTATAAAACACAGTTTAATGTCTTATTTCCAGCCAATGAGCATG

FLA305956 (K = G/T) (SEQ ID NO: 457)
CCTCAGGTTATCCACCCGCTTGGCCCCCTCAAAGTGTGGAATTACAGGTGTGAGCCACCGTGCCTGGC
CTGTTACATGTATAAAACACAGTTTAATGTCTTATTTCCAGCCAATGAGCATGGCTAGAGCAGCCTTG
GTCAAAGTTTGGTTTTTGGAGAAAATCCTTGTAGCTGACCTAAGATTCTCTTTGTGAGT

K

TAAGTAAGCACAGGTTGCAGAGAGGAGAAGGGTCTCTGGAGAGGTGTAATTTTCTAAATGGATTACAAG
TTCATGGACTTTTAACAGGTGTACAGGGGATAACAAGTTCTTTATAGACAGACTTTTGAGGACGTTTA
AGGGTATTCTGATTCTTGGTTTTCTAAGAGGGGAATGTATTATTTAACTACAGACACCCCTA

FLA306447 (Y = C/T) (SEQ ID NO: 458)
ATTCTAGACTCACTTTCTTTCTGTTTTTTTATTTTTTATTTTTTTTGGAGATGGAGCTTCACTCTGTCACC
AGGCTGGAGTGCAGTGGTGCAATCTTGGCTGACTGCAACCTTGCTTCCGGGCTTAAGCAATTTTTGT
GCCTCAGCCTCCTGAGTAGCTGGGATTACAGCATGCACCCACCATGTCCGGCTAATTTTTGTA

FIG. 8I

120/132

Y

CTTTAGTAGAGACAGGGTTTCACTATGCTGGCCAGCCTGGTCTCAAACCTCCTTACCTCAGGTGATCTGC
CCGCCTCGGCCTCCAGAGTGCTCAGATTACAGACGTGAGCCACTGGTGCCTGGCCTAGACTCACTTTC
AAGTGGCATAGACTTGTAAAATTATTTAAAGGTGATAGGTCTACAATGATCCTGTCAATTAG

FLA307155 (Y = C/T) (SEQ ID NO: 459)

AGAAAAATCCAGAATAATAAATTTGTCAATAGGAAAGACATTTCCACTGGGGGTTAAGAAGGAAGACA
TTGGAACAATGATAGCCACCACCTTATTGAATGCTTACTGTGAGCCAGGTGGCACTTCACCTTGTTCAT
TCTCACAACAGTCTAGGGAAGTAATTACTAATGTCTCCATCCACCTCTGTAGATGAGCAAA

Y

TGAGGCTCATTGAGGCTAGGAAATGCACCCACACTCACATAGCCATAAGAGGCAGCCATGGCATTGGG
CCCAGACCATGTGAACTTCAAAGACTACACGAGCAGCCACTGGGCAGCTGTATGGCTAAAGCCACTTG
AATTCAGCCCAGCAGCAACCCCTCTCCAGGAGGGGCACATAAGCTTGCAGCTTTGGGTAGA

FLA307165 (Y = C/T) (SEQ ID NO: 460)

GAATAATAATAATTTGTCAATAGGAAAGACATTTCCACTGGGGGTTAAGAAGGAAGACATTGGAACAAT
GATAGCCACCACCTTATTGAATGCTTACTGTGAGCCAGGTGGCACTTCACCTTGTTCATTCTCACAACA
GTCTAGGGAAGTAATTACTAATGTCTCCATCCACCTCTGTAGATGAGCAAACTGAGGCTCA

Y

TGAGGCTAGGAAATGCACCCACACTCACATAGCCATAAGAGGCAGCCATGGCATTGGGCCCAGACCAT
GTGAACTTCAAAGACTACACGAGCAGCCACTGGGCAGCTGTATGGCTAAAGCCACTTGAATTCAGCCC
AGCAGCAACCCCTCTCCAGGAGGGGCACATAAGCTTGCAGCTTTGGGTAGAAGCTGCACCT

FLA308514 (K = G/T) (SEQ ID NO: 461)

GCAGTTTGAAAATTCATCTTTGTTTTTACCTATATAATCACATGAAACCCGTGGTTCTCAAACGTCAG
CAGGCATCAGCATCACATGGAGGGCTTGTAAAACAGATTTCTGGGCCCCAACACAGAGTTTAAATTC
TGAAGGCTGAGGTGGGTGTGAACATTTGCATTTCTAACATGTTCTCGATGCTGCTGCCGCC

K

CTGGTCCCGAGAGCATGCCTGGAGAAGTGCCACCTTCGACCATGGACTGTGAGAATTCACATGGACCTC
AGAAATTATAATCAGTCTCTCAGTTTTACAGATAAGGAACTAAATCCAGAGAGATTGTTTTGCCAATGG
TGAACAGCTGGTTAAAGTCAGGATGGAGACTTTAATCCTAGTCAAGTGACCTTTCTCTGTGA

FLA308527 (K = G/T) (SEQ ID NO: 462)

TGCATCTTTGTTTTTACCTATATAATCACATGAAACCCGTGGTTCTCAAACGTCAGCAGGCATCAGCAT
CACATGGAGGGCTTGTAAAACAGATTTCTGGGCCCCAACACAGAGTTTAAATTCGAAGGCTGAGG
TGGGTGTGAACATTTGCATTTCTAACATGTTCTCGATGCTGCTGCCGCCCTCTGGTCCCGAGA

K

CATGCCTGGAGAAGTGCCACCTTCGACCATGGACTGTGAGAATTCACATGGACCTCAGAATTATAATCA
GTCTCTCAGTTTTACAGATAAGGAACTAAATCCAGAGAGATTGTTTTGCCAATGGTGAACAGCTGGTT
AAAGTCAGGATGGAGACTTTAATCCTAGTCAAGTGACCTTTCTCTGTATTTATTTCCCTCC

FLA309851 (R = G/A) (SEQ ID NO: 463)

GTGATCTGCCTGCCTCAGCCTCCCAAATTGCTGGGATTACAAGGCGTGTGTTTTAAGCCACTCAGTTT
GTGGCCACTTGTACAGCAGCAAGAGGAACTCATACAGTTATCATGTGAACCTCACAGGAATATGGTGA
GTTAAAAGAGAGGAAGGTGCAAAACATCCACGGTAGAGTGAGAACTCTCCAGGGAGTGAG

R

ACTGTGCCCAGCATACAGTGATCACCTCTTAGTAAGCTAAGTTTCTGAGCACCAGCTTTTTTGAGTTG
ACTTTGTGTCTTTAACATTTGAAGATCACCTTCTTTGCTCAGCCTGGCTTGAGACCTGGGCTGATT
TGTGGATCTGATAGAAAAGTTTCCTTAGTTGGGCTCTTCTCCCCGACCACCCCATGCCAGT

FLA311122 (R = G/A) (SEQ ID NO: 464)

CCACAGTTATCAGCAGCCACAGGCTTGACTTGAGCAAGTTGGAAGACAAATCAACTTCCAGAGTTGA
TTTAACATTGAGTGGAAATCAGTCATACTTTGGTCCCCCTTCGGGGCCACGCCTGGCACTGTGCCTGG
TGGCAGATCGGCATGAACCTGGCCAGCTTCTGTGGCCCTGGAGGGCACAGGCAGAAAGGCCAC

R

CTCAGTCCCATGATGAACCTGTTTAAAGACTTATTGTTGTCTCCCCGCTCTGTAAAGTAGATAGAGTGGAT
TTTATGTCCCTTATTACCTTTAGGATACTTTGACTCAGGGAGATAAAGTAACTTGGGTACAGCTACTC
AGCTGGTGAAGAACACAGGCAGAATGAGTGCCTGGGTCTTTTGACTTAAATTTCTGGATTTT

FLA311248 (S = G/C) (SEQ ID NO: 465)

FIG. 8J

121/132

CACTGTGCTGCTGGTGGCAGATCGGCATGAACTGGCCAGCTTCTGTGGCCCTGGAGGGCACAGGCAGAAAG
GCCACACTCAGTCCCATGATGAACTGTTTAAGACTTATTGTTGTCTCCCGCTCTGTAAAGTAGATAGA
GTGGATTTTATGTCCCTTATTACCTTTTCAGGATACTTTGACTCAGGGAGATAAAGTAACTTG

S

GTACAGCTACTCAGCTGGTGAAGAACACAGGCAGAATGAGTGCCTGGGTCTTTTGACTTAAAAATCTGG
ATTTTTCACAAAGATCCTCTTACTTTTATTTCATTACATAATAAATATATATTGAAGAGCTACTCTGTGC
CAAGCCCTGTGCCTAGATATACAGTGATAAATAAGAGTAGCTTCTAGAGGTCACCTGGCGG

FLA311737 (Y = C/T)

(SEQ ID NO: 466)

CCAAGTTCAGTGATAGAGAGCAGAGGTGAGGCGGCAGCAGAAACCACTTAAGGGACACCACGTGGCACT
CCTTCTGTGCTGAGAAGGCTGTGAGTAAGCTCACCATTATTTCTTATTTTCTCTCCTGAGTTAAATAG
GAAACATGTCTCGCATTACTTGAAAAATCAAGTCAAACCTATGCTCTTACTAGGAGTTATGGT

Y

CTTTTTATGTCTTAGATGATGCTTGATCTAGATGAATGCGGACTTGCTGTAGCTAGATAAATACAATGG
GAGTTTGAAGGTGTTTCGTAGCCCTGGAAATAGGTATTTCTGTCAAACAAGCTTTGTGCTAGTCCAGC
AGACAAAAGCATCAGTAACCTTGGTTGATAATCGTCATTTCTTAGGAATAAAGTAGACTGTA

FLA312038 (Y = C/T)

(SEQ ID NO: 467)

AGGTATTTCTGTCAAACAAGCTTTGTGCTAGTCCAGCAGACAAAAGCATCAGTAACCTTGGTTGATAA
TCGTCAATTTCTTAGGAATAAAGTAGACTGTAGAATTTTTTTTAGCAGAAAGGAAACCCAAAGATAATTC
TAGTGCAAATCCCTCACTTTATAGAGCAGAAGCTCAAGTCCCAGAGGAACAAGTGGCTTGAA

Y

GAACATCAGAATTTTAGGGGCTGGATTTGTACCCTCCTGGTGCCAGCAGCCCACTTCCCTGCAGGAGGC
ACTCACCTTCTTGCACAGGGGTATGAGTGTGGCCATTTCCACCCATAATCTCTGTTAGCTCATGTTT
AATTGGGTTCCCATTGAAAGAAAAATGGACCAGTAAGTTGGAGCAGAATCATTTCAGATGGTA

FLA312056 / SG13S30 (K = G/T) (SEQ ID NO: 468)

CAAGCTTTGTGCTAGTCCAGCAGACAAAAGCATCAGTAACCTTGGTTGATAATCGTCATTTCTTAGGAAT
AAAGTAGACTGTAGAATTTTTTTTAGCAGAAAGGAAACCCAAAGATAATTCTAGTGCAAATCCCTCACT
TTATAGAGCAGAAGCTCAAGTCCCAGAGGAACAAGTGGCTTGAACGAACATCAGAATTTTAG

K

GGCTGGATTTGTACCCTCCTGGTGCCAGCAGCCCACTTCCCTGCAGGAGGCACCTCACCTTCCCTGCACA
GGGGTATGAGTGTGGCCATTTCCACCCATAATCTCTGTTAGCTCATGTTCAATTGGGTTCCCATTGAA
AGAAAAATGGACCAGTAAGTTGGAGCAGAATCATTTCAGATGGTATAACATAAGGAAAACTT

FLA314532 (Y = C/T) (SEQ ID NO: 469)

GTGAGGCAAAAGTACTTTGTCGGTTACCTAGGAGAGAGAACGCAGAGGTAGGTAACCTGGGACTACTAAA
GAACTGTGGAGCGATTCTCGATTTTGTAGCAGGAAGAGTGACAATTCAAACAGTATTTGACTAGATTCT
ACGGCTCCGTAGCATCCCTTGGGTGGGAGGGGAAGGCTGACTAGGACCTCTGATTTCTTCT

Y

TCCCTGAGCTTTGAAGGCTCTGAAAAATACAGCTGGGGGGACTTGCCCACTTTTCTTATTAAGCAATTCC
TCCGCATGGTGTGCTGGCTTTCAAAGGGTGCTTCAGTGTCTGTTGCTGCACGTGCCTTGCAGCCCCACACC
CTGCACTCCCGCCCTGCAGAGTCTGGCGCTGGAATGACATTTTAGGTCTGGGTTCACAGGCC

FLA315014 (R = G/A) (SEQ ID NO: 470)

CATATCTTTTCAGGGACCAGAAGAAAGAAATGTTGGGAAAATAAGATGCAGTAAGATGCAGACATGACAGC
AGGGTGCAGCGGCTCAGGCCTATAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTG
AGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAAATATACAAA

R

CATTAGCCAGGCATGGTGGTGGGCGCCTGTAATCCAGCTACTCCATAGGCTGAGGCTGGAGAATCGCT
TGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAAAAG
CAAACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAGATGCAGACACGAGACTGTGA

FLA315232 (W = T/A) (SEQ ID NO: 471)

GGTGGGCGCCTGTAATCCCAGCTACTCCATAGGCTGAGGCTGGAGAATCGCTTGAACCCAGGAGGCAGA
GGTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAAAAGCAAACTCCATCTCAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAGATGCAGACACGAGACTGTGAAACTGACTAGCATCACC

W

TTGCATTGTTTATAGATGTTGCCAGACAGAAAGCCCCAAAGCAGCACAGTACCTTCTGACATCTGGAC
TAGGAATCTAGATTTTAGTAAAATACATGCTAATACTTACAGAAGAAATGTGGCGGTTAGAGTATGCC
GTCAGTTCCTTAGAGATTGCAATTCCTAATGCACTAGTATGGTTTCAGGTGCCAGGAACACG

FIG. 8K

122/132

FLA315355 (R = G/A) (SEQ ID NO: 472)

AAACTCCATCTCAAAAAAAAAAAAAAAAAAAGATGCAGACACGAGACTGTGAACTGACTA
GCATCACCATTGCATTGTTTATAGATGTTGCCAGACAGAAAGCCCCAAAGCAGCACAGTACCTTCCTGA
CATCTGGACTAGGAAATCTAGATTTTAGTAAAATACATGCTAATACTTACAGAAGAAATGTG

R

GCGTTAGAGTATGCCGTCAGTTCCTTAGAGATTGCAATTCCTAATGCACTAGTATGGTTTCAGGTGCCA
GGAACACGTTCTGTGAGGCTGCTGCCCCAGGTGCTGACCCAGCCTTCCACACCATTTCCTTCCTTGT
GTTACAGCCGCTCTGTCTTTTACAATAGCACCCCTCTCTAGTGGCTAATGGGCTCTATGAT

FLA315611 (K = G/T) (SEQ ID NO: 473)

GGTTTCAGGTGCCAGGAACACGTTCTGTGAGGCTGCTGCCCCAGGTGCTGACCCAGCCTTCCACACCA
TTTTCTTCCTTGTGTTTACAGCCGCTCTGTCTTTTACAATAGCACCCCTCTCTAGTGGCTAATGGGCT
CTATGATTAGATAGCATCCTTCAGTAGTGATAAAGGCAGTGACATCCTAGGGAGGTCAGCGG

K

TGAAAGCGCTATATCTGGAAACCTGAGAGCCTGTGAAGCTCAAGGACTTGACGGGGTTAGACCGTGAG
CCGGGCTGCAGCTGGAAAAAGAAATGACTGTTCTTTTACAGAGATCCTTCCCTGTGCCATCTCTTTCTTCA
TTCCTCTCTAGTGGCATTCTTATTTATCCTCTAAAACCACAATTCCATTATCTCTCCTATTCT

FLA316131 (S = G/C) (SEQ ID NO: 474)

AAGAGGGTCTTCTCTTTTGCCCTGGCTCCCTATGCAGCCCTATCTTACCCCTGCAAAGTCCCAGGGATG
TGGCTCAGTCACTGCTCCTCTCTTCATCTGTCCACTTGCTTGAGATCCTACAGCTGCTTTAATCCG
AGACCATCTGCAGAACATGACAAAATTTGTCCACCTACCCACATGTCTTTTAACTTTAAAG

S

CTTTACTAACTGATTCTTATTAGGGAATGAACAGAGGTGGCAAAAATAACAATAGGAGATTGATTTAC
AAGAAATCTTTAAAATAGTAGATTCTTCGGACCTCATTGAAATATAAATGGCCTGCCTTCTTGTGTCC
CTCCCTGGTCTCCCTCTTTAGGTGATAAGAAGAAGATCCTGCCAGCCCCATAACCCGCCATC

FLA316408 (M = C/A) (SEQ ID NO: 475)

CTTTAAATAGTAGATTCTTTCGGACCTCATTGAAATATAAATGGCCTGCCTTCTTGTGTCCCTCCCTG
GTCTCCCTCTTTAGGTGATAAGAAGAAGATCCTGCCAGCCCCATAACCCGCCATCTGCGCGGGTTCTAG
ACCCCTTCTCCTCCCTCTGGCCGTGGTAGGCATTACTGATGAATCATGGTGTCTTTCTT

M

CAGAGACCAAACCTGGCCTCGGAATCCTTCTTAACACAGATACTGCTTAACACAACCACTCTGAGCAGC
TGTCATAAGTAGAAGTAATAGATACTAGAAGAAATGTCTAAGCCTAATCTAGACCAAATACGGCCTGA
TATAGATGCAAGCCAGAGGGGCTTTATGGTTAAATGCAAGGAGATTTTCAACCTGCGCTCT

FLA316472 (R = G/A) (SEQ ID NO: 476)

CCCTGGTCTCCCTCTTTAGGTGATAAGAAGAAGATCCTGCCAGCCCCATAACCCGCCATCTGCGCGGGT
TCTAGACCCCTTCTCCTCCCTCTGCCCCTGGTAGGCATTACTGATGAATCATGGTGTCTTTCTTCC
AGAGACCAAACCTGGCCTCGGAATCCTTCTTAACACAGATACTGCTTAACACAACCACTCTG

R

GCAGCTGTCTAAGTAGAAGTAATAGATACTAGAAGAAATGTCTAAGCCTAATCTAGACCAAATACGG
CCTGATATAGATGCAAGCCAGAGGGGCTTTATGGTTAAATGCAAGGAGATTTTCAACCTGCGCTCTAG
AAGCTACTTGCTGAGATCTTCTTCAGTTGGGCCCATCTCCTCCCAGGCCTCTCTTCTGTTT

FLA316515 (M = C/A) (SEQ ID NO: 477)

CCCCATAACCCGCCATCTGCGCGGGTCTAGACCCCTTCTCCTCCCTCTGGCCGTGGTAGGCATTAC
TGATGAATCATGGTGTCTTTCTTCCAGAGACCAAACCTGGCCTCGGAATCCTTCTTAACACAGATACT
GCTTAACACAACCACTCTGAGCAGCTGTCTAAGTAGAAGTAATAGATACTAGAAGAAATGT

M

TAAGCCTAATCTAGACCAAATACGGCCTGATATAGATGCAAGCCAGAGGGGCTTTATGGTTAAATGCA
AGGAGATTTTCAACCTGCGCTCTAGAAGCTACTTGCTGAGATCTTCTTCAGTTGGGCCCATCTCCTCC
CCAGGCCTCTCTTCTGTTTCTGGGCTATGTACACTTGGACTCTGCAGACACCTAATGCTCT

FLA316569 (K = G/T) (SEQ ID NO: 478)

CGTGGTAGGCATTACTGATGAATCATGGTGTCTTTCTTCCAGAGACCAAACCTGGCCTCGGAATCCTT
CTTAACACAGATACTGCTTAACACAACCACTCTGAGCAGCTGTCTAAGTAGAAGTAATAGATACTAGA
AGAAATGTCTAAGCCTAATCTAGACCAAATACGGCCTGATATAGATGCAAGCCAGAGGGGC

K

TTATGGTTAAATGCAAGGAGATTTTCAACCTGCGCTCTAGAAGCTACTTGCTGAGATCTTCTTCAGTT
GGGCCCATCTCCTCCCAGGCCTCTCTTCTGTTCTGGGCTATGTACACTTGGACTCTGCAGACACCT
AATGCTCTTGGGACCTGCTTTAGTTCTTGACCTCACCAACCGAGGAGGAATTGCTAGATGAG

FIG. 8L

123/132

FLA316607 (Y = C/T) (SEQ ID NO: 479)

TCCAGAGACCAAACCTGGCCTCGGAATCCTTCTTAACACAGATACTGCTTAACACAACCACTCTGAGCA
GCTGTCATAAGTAGAAGTAATAGATACTAGAAGAAATGTCTAAGCCTAATCTAGACCAAAATACGGCCT
GATATAGATGCAAGCCAGAGGGGCTTTATGGTTAAATGCAAGGAGATTTTCAACCCTGCCGT

Y

TAGAAGCTACTTGTCTGAGATCTTCTTCAGTTGGGCCCATCTCCTCCCCAGGCCTCTCTTCTGTTCTCGG
GCTATGTCACACTTGGACTCTGCAGACACCTAATGCTCTTGGGACCTGCTTTAGTTCTTGACCTCACCA
ACCGAGGAGGAATTGCTAGATGAGATCCTTCCCCCGGAATTTCTCTCTTGAACCCAGATGG

FLA316763 / SG13S32 (M = C/A) (SEQ ID NO: 480)

AGGGGCTTTATGGTTAAATGCAAGGAGATTTTCAACCCTGCCGTCTAGAAGCTACTTGTCTGAGATCTTC
TTCAGTTGGGCCCATCTCCTCCCCAGGCCTCTCTTCTGTTCTCTGGGCTATGTCACTTGGACTCTGCA
GACACCTAATGCTCTTGGGACCTGCTTTAGTTCTTGACCTCACCAACCGAGGAGGAATTGCT

M

GATGAGATCCTTCCCCCGGAATTTCTCTCTTGAACCCAGATGGTCCGTTGCCCTTTCCAGAAGTTGC
TCCAGCCCTGTCCGCTTAGGAAGTTTCAGTGTCTCCTTGATCCAGTGGGTAGGGAAGACATTCCATAAT
GAATGCCCCAGTCTGAGCTTCTTCTCAGGCTTCAGGCTGCCCTGCGAGGATTTTGCAGCT

FLA317496 (R = G/A) (SEQ ID NO: 481)

GAGTAGCTGAGACTACAGGTGTGCACTACCACACCCAGCTAATTTTTGTATTTTTAGTAGAGATAGGG
TTTAGCTATGTTGGCCAGGCTGGTCTCGAACTGCTGAACCTCAAGCAATCTGCCATCCCCGGCCTCCCAA
AGTACTGGGAGTATAGGCATAAGCCACCCATGATGCCAGCCTGAATCTTGGTTTCTTCCCC

R

TTCATTTAAGCTATTACCTGGGCTGAACTCAATGGCACCTGGCACCAACTGGCAACTGACTCTTGGTC
TTTTATTACCTACCTTCCCTAGCAGGCACTGGGTTGCTCCCTCTTCTATCCCATGGAGTCTGTCTCT
TGTTGGGGCTCCTACTGATCCTCTTGGCAATATGAAGTTCTCAGCTCAATGGTGGGTGGGCA

FLA317619 (R = G/A) (SEQ ID NO: 482)

TCCCCGGCCTCCCAAAGTACTGGGAGTATAGGCATAAGCCACCCATGATGCCAGCCTGAATCTTGGTT
TCTTCCCCATTCAATTTAAGCTATTACCTGGGCTGAACTCAATGGCACCTGGCACCAACTGGCAACTGA
CTCTTGGTCTTTTATTACCTACCTTCCCTAGCAGGCACTGGGTTGCTCCCTCTTCTATCCC

R

TGGAGTCTCTGCTCTGTTGGGGCTCCTACTGATCCTCTTGGCAATATGAAGTTCTCAGCTCAATGGTG
GGTGGGCAATGACTGCCAATCTTGGAGGCAATGAACCTCAGGTTACCCCACTCCTCCTCCTGAGTT
GCTCACTCACTCCTCATTCACTCAACATTGATTTCAGTAGATATTTGCTACCTGCTCTGTGCC

FLA317620 (Y = C/T) (SEQ ID NO: 483)

CCCCGGCCTCCCAAAGTACTGGGAGTATAGGCATAAGCCACCCATGATGCCAGCCTGAATCTTGGTTT
CTTCCCCATTCAATTTAAGCTATTACCTGGGCTGAACTCAATGGCACCTGGCACCAACTGGCAACTGAC
TCTTGGTCTTTTATTACCTACCTTCCCTAGCAGGCACTGGGTTGCTCCCTCTTCTATCCCA

Y

GGAGTCTGTCTCTGTTGGGGCTCCTACTGATCCTCTTGGCAATATGAAGTTCTCAGCTCAATGGTGG
GTGGGCAATGACTGCCAATCTTGGAGGCAATGAACCTCAGGTTACCCCACTCCTCCTCCTGAGTTG
CTCACTCACTCCTCATTCACTCAACATTGATTTCAGTAGATATTTGCTACCTGCTCTGTGCCA

FLA317647 (Y = C/T) (SEQ ID NO: 484)

TAGGCATAAGCCACCCATGATGCCAGCCTGAATCTTGGTTTCTTCCCCATTCAATTTAAGCTATTACCT
GGGCTGAACTCAATGGCACCTGGCACCAACTGGCAACTGACTCTTGGTCTTTTATTACCTACCTTCCC
TAGCAGGCACTGGGTTGCTCCCTCTTCTATCCCATGGAGTCTGTCTCTGTTGGGGCTCC

Y

ACTGATCCTCTTGGCAATATGAAGTTCTCAGCTCAATGGTGGGTGGGCAATGACTGCCAATCTTGGAG
CCAATGAACCTCAGGTTACCCCACTCCTCCTCCTCTGAGTTGCTCACTCACTCCTCATTCACTCAACAT
TGATTTCAGTAGATATTTGCTACCTGCTCTGTGCCAGGTACCAGGTGAGTTGCTGAAGGAGTA

FLA317733 (W = T/A) (SEQ ID NO: 485)

CACCTGGCACCAACTGGCAACTGACTCTTGGTCTTTTATTACCTACCTTCCCTAGCAGGCACTGGGTTG
CTCCCTCTTCTATCCCATGGAGTCTGTCTGTGGGGCTCCTACTGATCCTCTTGGCAATATGAA
GTTCTCAGCTCAATGGTGGGTGGGCAATGACTGCCAATCTTGGAGGCAATGAACCTCAGGT

W

FIG. 8M

124/132

CCCCACTCCTCCTCCTCCTGAGTTGCTCACTCACTCCTCATTCACTCAACATTGATTAGTAGATATTT
GCTACCTGCTCTGTGCCAGGTACCAGGTCAAGTTGCTGAAGGAGTAACAGTGAACATGACGGAGTCTTTG
TCCCCAAGGAGACCCAAGGTGTCTCCTAGAGCCAGGGGCACATTGCAAGACCAAAATATATTT

FLA317744 (Y = C/T) (SEQ ID NO: 486)
AACTGGCAACTGACTCTTGGTCTTTTATTACCTACCTTCCCTAGCAGGCACTGGGTTGCTCCCTCTTCC
TATCCCATGGAGTCTGTCTCTGTGGGGCTCCTACTGATCCTCTTGGCAATATGAAGTTCTCAGCTC
AATGGTGGGTGGGCAATGACTGCCAACTCTTGAGGCCAATGAACTCAGGTTACCCCACTCCT
Y
CTCCTCCTGAGTTGCTCACTCACTCCTCATTCACTCAACATTGATTAGTAGATATTTGCTACCTGCTC
TGTGCCAGGTACCAGGTCAAGTTGCTGAAGGAGTAACAGTGAACATGACGGAGTCTTTGTCCCCAAGGAG
ACCCAAGGTGTCTCCTAGAGCCAGGGGCACATTGCAAGACCAAAATATATTCAACTTACCAAA

FLA317815 (R = G/A) (SEQ ID NO: 487)
TCCCATGGAGTCTGTCTCTGTGGGGCTCCTACTGATCCTCTTGGCAATATGAAGTTCTCAGCTCAA
TGGTGGGTGGGCAATGACTGCCAACTCTTGAGGCCAATGAACTCAGGTTACCCCACTCCTCCTCCTCCT
GAGTTGCTCACTCACTCCTCATTCACTCAACATTGATTAGTAGATATTTGCTACCTGCTCT
R
TGCCAGGTACCAGGTCAAGTTGCTGAAGGAGTAACAGTGAACATGACGGAGTCTTTGTCCCCAAGGAGAC
CCAAGGTGTCTCCTAGAGCCAGGGGCACATTGCAAGACCAAAATATATTCAACTTACCAAAATAATCATA
GACCTAGTTCTCAAAAAGCAAGAAGACTGATTCTCGTTGTCTTTCTCCTCCTCAGCATCA

FLA318219 (W = T/A) (SEQ ID NO: 488)
TTTTAGAGTCTGTGGGCCCCCTCCAAGTGTGGAGTATGGTGTACTTACCAGAGTTTGAGGAGAAACAT
TCTTCTTTTGAAGGCCGGGGAGCATAGATGGATATCAAGGCTGCTGTTTCTAAAGCCGAAACCCACCA
AACAACAGTATTAGAATCATCTGTGGTGTCTTATTAAAGATACAGATTCTTGGGCCCCATCCC
W
GACTTATGAATCAGAATCTCTGCCAGAGGAAGCCTGAGAATTTGCATTCTCAGATGATTCTGCATTCTC
AGATAACACATTCTTTAGGTGATTCTTACACACACTGGAGTTTGGGAATCGCTGAAGGCTGTTCACTTC
TCTTTTCTGAGAAATGATTCAATTCATTTAGAAATATTTGAGAGGTCCTTATTTATTGGAG

FLA319969 (K = G/T) (SEQ ID NO: 489)
GGTGGCCTCATTCTGTGTATAAATCTGAGCCACCACGATATTTGACTTTTACAAATTTAATTTATCTGA
ACCCTCTATTCTCTGGCTAAAAAATATCCCTTACTTGGACTTCTTTATTTTATTTTCAATTCCTTACC
AGCACTAGCAGGGGACTCTGTACTCATCTGCTGGCGCTGCCATAACAAAGCACTGCAGCCTG
K
GGGGCTCAAACCACAGAATTTATTCTCTCACAGTCTTAGAGGCTAGAAGTCCAAGATCAAAGTGTGGGC
AGGGTCGGTTTCTCCTGCAGCCTCTCTCCTTGGCTTATAGAGTGCCACCTTCTACCTGTGTCTTCACAT
CATCACCTCACTGAGCATGTCTGTGTCAAATCTCCCTTCTTATAAGACCCCAAGTCATACT

FLA320261 (R = G/A) (SEQ ID NO: 490)
TCTCTCCTTGGCTTATAGAGTGCCACCTTCTACCTGTGTCTTACATCATCACCTCACTGAGCATGTCT
GTGTCCAAATCTCCCCTTCTTATAAGACCCCAAGTCATACTGGATGAGGATCCACCCATATGAGTTCAAT
TTACCTTAATTATCTCTTTAAACACCCTGTCTCAAATACAGTCCCATTCTGAGGAACCTGAG
R
GTAAAGATTCAACATATGAATTTTGAAGGGACCTAATTCAGCCCACAACACCCTCTTTTGGGATGTTT
ATTTTCCCCCTTAAGGAGCTAGTTAGGATGTCTTATCTCATGAACATGACTGTGAACAGGAAAACAGGG
AGAGAATGAAGCTGGCCAAGGAACAGGGCTGGTGTGAGCTAGCAGTGCTTTTCTGATGTGAG

FLA320393 / SG13S42 (R = G/A) (SEQ ID NO: 491)
TTCATTTTACCTTAATTATCTCTTTAAACACCCTGTCTCCAAATACAGTCCCATTTCTGAGGAACCTGAGA
GTAAAGATTCAACATATGAATTTTGAAGGGACCTAATTCAGCCCACAACACCCTCTTTTGGGATGTTT
ATTTTCCCCCTTAAGGAGCTAGTTAGGATGTCTTATCTCATGAACATGACTGTGAACAGGAAAACAGGG
R
ACAGGGAGAGAATGAAGCTGGCCAAGGAACAGGGCTGGTGTGAGCTAGCAGTGCTTTTCTGATGTGAGT
GGGTCCACAGGGAGCTTGTAAATGCAGATTCTGATTCAATAGGTTCCAGAGGGACCTGAGATTTC
CATTTCTGACAAGTTTCCAGTGTGGGGCTGATGCTGCTGGTCCACGGACCATACTTTGAGT

FLA320595 (K = G/T) (SEQ ID NO: 492)
CAGGGAGAGAATGAAGCTGGCCAAGGAACAGGGCTGGTGTGAGCTAGCAGTGCTTTTCTGATGTGAGTG
GGTCCACAGGGAGCTTGTAAATGCAGATTCTGATTCAATAGGTTCCAGAGGGACCTGAGATTTC
ATTTCTGACAAGTTTCCAGTGTGGGGCTGATGCTGCTGGTCCACGGACCATACTTTGAGTA

FIG. 8N

125/132

K

CAAGGAGCTTGATACATAATGGCTGAGTGACTTTTCAGACTCCTGCTGTAGAAAAATTA1 3AGTTGGCTG
GGCGTGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTCAG
GAGTTTCGAGACCAGCCTGGCCAACATGGTGAAACACCATCTCTACCAAAAATACAAAAATTA

FLA321774 (Y = C/T) (SEQ ID NO: 493)

TCACTTAAGCCCAGAACTGAGGTTGCAGTGAGCCGAGATTGCACCACTGCACTCCAGCTTGGGCTAC
AGAGTGAGACTCTATCTCAAAAACAAAGAAAACAAACAACAATAACAACAAAAACCAAGTCTCTCCC
TCCACTCAAAAATGCAAGGGCCTGTCTCCCATTTGCTGGGTGCCAGGTCTCATGAATGTAGA

Y

ATGAATTATTCCAGTCAGCCTCAGGAGAATAGAATGAGCCCTCAGATGCCGAAGCACCTTTTCAGATTCC
ACCGGTTTTATCGGCTCATTTAACTTCATTCTAACACAGTCCTGCATTACACACGTGTCTGTCGTTA
TGGGCAGCTGCAGAGAGGGTCTTAATGGTCCTAATGCTCAGTGAGGATGCCCAATGGTCAAC

FLA321966 (R = G/A) (SEQ ID NO: 494)

AATGTAGATATGAATTATTCCAGTCAGCCTCAGGAGAATAGAATGAGCCCTCAGATGCCGAAGCACCTT
TCAGATTCCACCGGTTTTATCGGCTCATTTAACTTCATTCTAACACAGTCCTGCATTACACACGTGT
CTGTCTGTTATGGGCAGCTGCAGAGAGGGTCTTAATGGTCCTAATGCTCAGTGAGGATGCCCA

R

TGGTCAACAGAACCTGCCATCTTCAGGCCATCAAGGAGCTCTGGAGTTAAGGAAATCATGAGAGCACAG
AGGGGCGGGTACAGCAGAGCCCTCGTGGTAATGGGTTTTGAGGTCTAGGCTCTCTTCATTGGGTTTGA
AATAAGTTCAATGACTAGTAATAGCTGAGACACTTCTACCCCTCAAATGAAGTAAATGGGAA

FLA322025 (W = T/A) (SEQ ID NO: 495)

GAAGCACCTTTTCAGATTCCACCGGTTTTATCGGCTCATTTAACTTCATTCTAACACAGTCCTGCATT
ACACACGTGTCTGTCTGTTATGGGCAGCTGCAGAGAGGGTCTTAATGGTCCTAATGCTCAGTGAGGATGC
CCAATGGTCAACAGAACCTGCCATCTTCAGGCCATCAAGGAGCTCTGGAGTTAAGGAAATCA

W

GAGAGCACAGAGGGGCGGGTACAGCAGAGCCCTCGTGGTAATGGGTTTTGAGGTCTAGGCTCTCTTCAC
TTGGGTTTGAAATAAGTTCAATGACTAGTAATAGCTGAGACACTTCTACCCCTCAAATGAAGTAAATGG
GAAAATGGAGCATTGTTGAGTCCAGGGAGCTATAATTTAAACCCCATATATCTAAAAGGGGT

FLA322093 (R = G/A) (SEQ ID NO: 496)

TACACACGTGTCTGTCTGTTATGGGCAGCTGCAGAGAGGGTCTTAATGGTCCTAATGCTCAGTGAGGATG
CCCAATGGTCAACAGAACCTGCCATCTTCAGGCCATCAAGGAGCTCTGGAGTTAAGGAAATCATGAGAG
CACAGAGGGGCGGGTACAGCAGAGCCCTCGTGGTAATGGGTTTTGAGGTCTAGGCTCTCTTC

R

CTTGGGTTTTGAAATAAGTTCAATGACTAGTAATAGCTGAGACACTTCTACCCCTCAAATGAAGTAAATG
GGAAAATGGAGCATTGTTGAGTCCAGGGAGCTATAATTTAAACCCCATATATCTAAAAGGGGTAAACATT
TTTGTGTGTGTGAAATGGGTGTCATTGCACTGCATCTACAGTTTTCTTTTTCTTCTCTTC

FLA323013 (R = G/A) (SEQ ID NO: 497)

ATTTATCTCTATACCCACAAACGACTAGTTTGTTCCTCAAACCTAAATGATAATATTAATAATACACA
TCCTGGCCAGGTGTGGTGGCTCATACCTGTAATCCAGCACTTTGGGAGGCCGAGGCAGGTGGATCACT
TGAGGTCAGGAATTAAGACCAGCCTGGCCAATATGGTGAAAGCCTGTCTGTACTAAAAATAC

R

AAAATTAGCCAGGTATGCTGGTGGATGCTTATAATCCAGCTACTTGGGAGGTTGAGGCAGGAGAATTG
CTTGAACCCGGGAGGTAGAGGTTGCAGTGAGCCAAGATCATGCCACTGCACTCCAGCTTGGGCAACAGA
GTGAGACTCCATCTCAAATTAATAAATAACACATCTGGCTTCTGGAAAAATTAATTGAAGA

FLA323316 / SG13S34 (K = G/T) (SEQ ID NO: 498)

AAGATCATGCCACTGCACTCCAGCTTGGGCAACAGAGTGAGACTCCATCTCAAATTAATAAATAACAC
ATCTGGCTTCTGAAAAATTAATTGAAGATCTTTATGACATCCATCCCTCTTCACACAGCCATGTGAA
TTAGGTTGGTATCTTCATATACTAGCATCGTGCCAGCACTTCCATGTTATACAGTTTAAAA

K

GTTCTGTAATTCCTGTGGGAACCTAAGATAATGCGAGGACCGTCATACGTGCCCCCAATATTGGCAA
ACCAATGAATAAATGAATGAATGAGTTTATGAATCGCTAACTGGCTGTATTTAATGAAGTATGTGTGT
GAGCCATTTCCACAGTGTGGACAGATTTGTCCCAATATGGGCCTCTTCCCAAAGGCCCT

FLA323366 (R = G/A) (SEQ ID NO: 499)

FIG. 80

126/132

CAAATTAATAAATAACACATCTGGCTTCTGGAAAAATTACTTGAAGATCTTTTATGACATCCATCCCT
CTTCACACAGCCATGTGAATTAGGTTGGTATCTTCATATACTAGCATCGTGCCAGCACTCCATGTTA
TACAGTTTAAATGTTCTGTAATTCCTGTGGGAACCTAAGATAATGCGAGGACCGTCATAC

R

TGCCCCCAAATATTGGCAAACCAATGAATAAATGAATGAATGAGTTTATGAATCGCTAACTGGCTGTAT
TTAATGAAGTATGTGTGTTGAGCCATTTCCACAGTGTGGACAGATTGTGCCACAATATGGGCCTCTT
CCCCAAGGCCCTACCACCTAATGCCATCACACTGGGGATTGTGATTCAACATGTGAATTTGG

FLA324591 (R = G/A) (SEQ ID NO: 500)

GTGATACTTTATTTATGTGTGTGGATTGTGTAATGATGAAGTCAGGGCATTAGGGTCTTCATCACCTTG
ATTATCATTTCTATGTGTGTGAGAACATTTCAAGTTCTCAGTTCCAGCTATTTTGAAATAGACAGTCCAT
TTTGTGTAGCTACAGTCACCCAACCCGGCTGTCAGACATTGGAACCTACTCCTATTGAACCTGT

R

TATTTGTACCCATTACCAAACCTCTCTTTGGGCTTTTCAGTTTACAACTGGGATGATCCTGGGAAAACT
AAAGTAAATCAGACACCCGACGTGTGAGCTAGGTTATAATATGCCAGTGGACCCTGGGGACATCTTAG
CTTTTCAGAGGTCATGCTGTCCAAGCTGACTGTGGGGCTTCAGAAGGTGGGGAGAGGAAATG

FLA324601 (Y = C/T) (SEQ ID NO: 501)

ATTATGTGTGTGGATTGTGTAATGATGAAGTCAGGGCATTAGGGTCTTCATCACCTTGATTATCATTT
CTATGTGTGTGAGAACATTTCAAGTTCTCAGTTCCAGCTATTTTGAAATAGACAGTCCATTTTGTGTAGCT
ACAGTCACCCAACCCGGCTGTCAGACATTGGAACCTACTCCTATTGAACCTGTGTATTTGTAC

Y

CATTACCAAACCTCTCTTTGGGCTTTTCAGTTTACAACTGGGATGATCCTGGGAAAACTAAAGTAAATC
AGACACCCGACGTGTGAGCTAGGTTATAATATGCCAGTGGACCCTGGGGACATCTTAGCTTTTCAGAGG
TCATGCTGTCCAAGCTGACTGTGGGGCTTCAGAAGGTGGGGAGAGGAAATGATGCAATGGC

FLA324849 (S = G/C) (SEQ ID NO: 502)

CCTGGGAAAACTAAAGTAAATCAGACACCCGACGTGTGAGCTAGGTTATAATATGCCAGTGGACCCTG
GGGACATCTTAGCTTTTCAGAGGTCATGCTGTCCAAGCTGACTGTGGGGCTTCAGAAGGTGGGGAGAGG
AAATGATGCAATGGCCCATCAGAGGCCTACTTGGGGCTTGGGGCCAGAGTGCATGTCTAAG

S

CATTAAGGGGAGGGGAGAGCAGCCTTCATAATTATGAAGAGGAGTCTCAGGTGCACAGCTTCTGATGAG
GGACAGCTTCTAATTGAAGACAGCATTTGTGTAATGCTCAAACCTCCCTGTCTTCAGAGTGCCTGTCTAT
CCCACCATCAGTTCTGTGACTTCTCCCTAAGCCTCAATTTTGCATGTGTTACATTGGGATAA

FLA325369 (Y = C/T) (SEQ ID NO: 503)

TTCTTGTCATAGCAAATCTTGCAAATGTAGGGACTCAAACAATATAAATTTATTATCTGACAGTTTTT
CTGGGTGACAGGCTTCTACTAGGCTGTAATCAGAGGGCAACCAAAGCTGTGATCTCAGCTGAAGCTCAGG
ATTCTCTTCCAAGCTCACTGGTTGTTGGCAGAATTTCAGTTCTTTCCAGTTGGAAGACTAAAG

Y

CTACAGTCTTTCAGTCTCTAGAAGCCTTTTCTCTGGCACAGGTTTCTCTACAACATGGCCATTTATGTCT
TTAAGGCCAATAGGAGAACATGATTAGCATATTTTTTTTAAAGTGAACCTTTAGACCCTTTTTTAAAGGCC
TATCTGATTAGGCCAGGCCCAAGTGAGCTTTAAGTCAACTGATTAGAGATCTTAATTACATC

FLA326187 (R = G/A) (SEQ ID NO: 504)

CTGGGATTACAGACACACACTGCCACGCCTGGCTAATTTTTGTATTTTTTAGTAGAGACGAGGTTTTGCC
ATGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAAGTGATCCGCCCACCTCAGCCTCCCAAAGTGCTG
GGATTACAGACGTGAGCCACCATTAAACATTTTTCTATCTCCTGTGGGAAGGGCACAGTGA

R

AGAACAGATGAAGCTGAGACATACAAGTGAACCTCTCCCTCCTCTCCATTTAGACTAAAATAGGATTAT
TCATACTGAGATTCTCCCTGGTTGCAAAGAGATAATCTGTGCAACTGGGTTTTTACAATTATCCCTACC
CTATGCTTTCTCATCTGTCTTCTCGTAGTCAGCTCAGGCTGCTATAACAAAACACCATAA

FLA326657 (R = G/A) (SEQ ID NO: 505)

CTGGCAGATTCCGTGTCTAATGAGGTCTGCTTTCCAGTTTATAGACAGTGCCTTATCGCTACCGCCTT
ACACAGTGAAGGAGAGGACGAGAAGCTCCTTGGGCTTTTTTTTTGTTTCTTTCTCTCTCTCTC
TTTTTTTTTTTTTTAATAAGGTCACTATCTTAGTCCATTTTGTGTTGCTAAAAGGAACATCT

R

AGGTTGAGTAATTTATTTTATTTTAAAAAGTGGCCAGGCATGGAGGCTTATCCTGTAAACCTAATCCTT
TAGGAGGCCAAAACAGCAGGATTGTTTGGAGCCAGGAGTTCAAGACCAGCCTAGGCAAGATAGTGAGAC
CCCATCTACCCCATCTCTACTAAAATTTTAAAAAATTAGCTGTGTGTTGTAAAGTGTGCTTG

FIG. 8P

127/132

FLA327265 (Y = C/T) (SEQ ID NO: 506)

TCATGGGGGAAGACGAAGGAGAGCTGGCACGTGCAGATATCACGTGTTGAGGGCAGAAGCGAGAGAGAG
AGGGGAGAGATGCCAGGCTCTTTTTTAACAACCAGCACTGGGGAACTAATAGAGTGAGAGCTCACTGAC
TCCTGAGGGAGGACATTAATCTATTGATGAGCGACCTGCCTCCATGACCCAAACACCTCCAA

Y

GATACCCACCTCCAACACTGCCACACTAGGGATTAACCTTCAACTTGAGATTTAGAGGGGGGAACTT
ACAACTATCGCAGGCACTAATACCACTCATGAGGGCTCCACCTTCATGACCTAATCACTTCCTAAAGG
CCTTACCTCTTAATCTCATCACATTGAGGATTCGATTTCAACTTGAATTTTGGGGGGACACC

FLA328964 (Y = C/T) (SEQ ID NO: 507)

AACCTGTCTTAAACATGAAAGTTCCTTAGTGCTACCCCCAGAGGTATGATTTGGTAGGTCAAGGATAG
GGCCTGGAAATTCACATTCTTGTTAAGATGTTCTTCATCCGGGGTTTGTGACCACCTTTTCAGAAGAT
TTTTGCTCTGTAGCTGTACTACCCAATGCAGTAGTTCGTAGTCAGTGTGGCTCCTGAGCCCT

Y

GAAGTGTAGCTCCTCTGAACTGAGACGTGCTGTAAATGTAAATTCACACCGGAGTTTGAAGAGTTAAT
ACAAAGAAAAGGAATGCAAAACATCTCATTAAATAATGCTTTACACTGATTACATATTGAAATGGTAAT
CTTGTAGATATAGTGCCTTAAATAAAATATACTGTTAGGCTTAATTTACAGTCTTTTATACTT

FLA330265 (Y = C/T) (SEQ ID NO: 508)

ATTACGCCAATCAACAAGAGGGCAAAAGAACAACATTTGATGTGTAATTACTTAATTTAGTGCATATG
CATTTGGGTCTCTCAATGTGAGCACTATGGCAACCAGAACATGGCCACAATAACTGTCTGGAAATGTCTA
TTCTTACCTGGACCCAGCAGGCCATGCCCCACTGATTATATAATCTCCCTCTCTCCTTGTTA

Y

GGTCTGAATGCTTGCATCCCTCAAAAATTCATGTGTTGAAATCCTAACCCCCAAGGTGATGATATTAGG
AGGTCCGGCCTTTTGGAGAGGTAATTAGGTCATGAAGACAGCATCCTCATGAATGGGATTAGTGTCTTAT
AAAATAGGCCCAAGGGAGCTCATTCATTTGTCCACCATGTGAGAACACAGCGAGAGGGCAC

FLA330455 (Y = C/T) (SEQ ID NO: 509)

CTCCTTGTTACGGTCTGAATGCTTGCATCCCTCAAAAATTCATGTGTTGAAATCCTAACCCCCAAGGTG
ATGATATTAGGAGGTGGCCTTTTGGAGAGGTAATTAGGTCATGAAGACAGCATCCTCATGAATGGGATT
AGTGTCTTTATAAAATAGGCCCAAGGGAGCTCATTCATTTGTCCACCATGTGAGAACACAG

Y

GAGAGGGCACCATTATGCACCAGGAAATGGGCCTTTTCCAGACAATCTGTGCGTGCCTGGATCTTGGA
CTTCACAGCCTCTAGAATGTGAGAAATTAATTTGTTTTTTTATAAGCCACCAATCTATGGTTTTTTTT
ATAGAAACCGTAATGGACTAAAACACTCCCTAATTATATTTAACTTATCAGTGCCTGAGG

FLA331234 (R = G/A) (SEQ ID NO: 510)

GACAGGTAGGCAAGGAGGTGGGTGTCAGGGGAGTTGAGGGTTGCCTGTGTACTTTTCTAGACTGTTCC
ACTTCACATCAGTGAAATATTCCCAATTGATACTATCATGAAACAAAGCAAATGAAATGCTGAGCAGG
AGCTTCGTCTTGATGAAATGCTGAAAGAAAAGAAAGGAAAAATAAAGTAGCCATTATTTTTT

R

CCCTTCCTCCACCCCCATGTTTACTACTCTTATTTCTCTTTTGTATTGTTGTGTTGGAAGCACAGCAT
CAGAAAAAATCCAGTTTTGAGAGATAACTCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGAGG
ATGCCACCGTGAGGTCCAGGACGTAAAGAGGAAAAAACAGACAAAAAATCCATATGAAAT

FLA331374 (Y = C/T) (SEQ ID NO: 511)

GCTTCGTCTTGATGAAATGCTGAAAGAAAAGAAAGGAAAAATAAAGTAGCCATTATTTTTTGCCCTTCCT
CCCACCCCATGTTTACTACTCTTATTTCTCTTTTGTATTGTTGTGTTGGAAGCACAGCATCAGAAAAA
CTCCAGTTTTGAGAGATAACTCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGAGGA

Y

GCCACCGTGAGGTCCAGGACGTAAAGAGGAAAAAACAGACAAAAAATCCATATGAAATGAAATGTG
AAAGAGGCGCTTTCGAGCAGATGAGTGTGTTGATGATTACAGTGTGAGAGCTGTTTGTGTCCAGAGCTGC
TTGCTGCACCTGGCGGGATAAACACTGGTCTAACAGAGGATCCTTGTTCAGGAGGCTGCC

FLA331395 (R = G/A) (SEQ ID NO: 512)

GAAAGAAAAGAAAGGAAAAATAAAGTAGCCATTATTTTTGCCCCTTCCTCCACCCCATGTTTACTACT
CTTATTTCTCTTTTGTATTGTTGTGTTGGAAGCACAGCATCAGAAAAAATCCAGTTTTGAGAGATAAC
TCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGAGGATGCCACCGTGAGGTCCAGGAC

R

TAAAGAGGAAAAAACAGACAAAAAATCCATATGAAATGAAATGTGAAAGAGGCGCTTTCGAGCAGA
TGAGTGTGTTAGATTACAGTGTGAGAGCTGTTTGTGTCCAGAGCTGCTTGCTGCACCTGGCGGGATAA
ACACTGGTCTAACAGAGGATCCTTGTTCAGGAGGCTGCCTTTTATTTGGGGGGACAAAT

FIG. 8Q

128/132

FLA331473 (R = G/A) (SEQ ID NO: 513)

CTTTTGTATTGTTGTGTTGGAAGCACAGCATCAGAAAACTCCCAGTTTTGAGAGATAACTCAGTGTTT
AGTTCACTTAAACCTGAGAAAGGAGAAGAGGATGCCACCGTGAGGTCCAGGACGTAAAGAGGAAAAAA
CAGACAAAAAATCCATATGAAATGAAATGTGAAAGAGGCGCTTTCGAGCAGATGAGTGTT

R

TAGATTACAGTGTTGAGAGCTGTTTGTGTCCAGAGCTGCTTGCTGCACCTGGCGGGATAAACACTGGTC
TAACAGAGGATCCTTGTTTCAAGGAGGCTGCCTTTTATTGGGGGGACAAAATTGTTCTTGAAAGCTGC
TCAGTGGTTCAAGCTACAGCATGGTGGACTAGCAGAATGGACTCCAGGGCCTCCGAGGAGAC

FLA331517 (Y = C/T) (SEQ ID NO: 514)

AGTTTTGAGAGATAACTCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGAGGATGCCACCGTGAG
GTCCAGGACGTAAAGAGGAAAAAACAGACAAAAAATCCATATGAAATGAAATGTGAAAGAGGCGCT
TTCGAGCAGATGAGTGTTGTAGATTACAGTGTTGAGAGCTGTTTGTGTCCAGAGCTGCTTGCT

Y

GCACCTGGCGGGATAAACACTGGTCTAACAGAGGATCCTTGTTTCAAGGAGGCTGCCTTTTATTGGGG
GGACAAAATTGTTCTTGAAAGCTGCTCAGTGGTTCAAGCTACAGCATGGTGGACTAGCAGAATGGACTC
CAGGGCCTCCGAGGAGACAGTGACTGCTGCCAGAAATAGTCAAGGATAGAAAGGAAGGACTT

FLA331526 (Y = C/T) (SEQ ID NO: 515)

AGATAACTCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGAGGATGCCACCGTGAGGTCCAGGAC
GTAAAGAGGAAAAAACAGACAAAAAATCCATATGAAATGAAATGTGAAAGAGGCGCTTTCGAGCAG
ATGAGTGTTGTAGATTACAGTGTTGAGAGCTGTTTGTGTCCAGAGCTGCTTGCTGCACCTGG

Y

GGGATAAACACTGGTCTAACAGAGGATCCTTGTTTCAAGGAGGCTGCCTTTTATTGGGGGGACAAAAT
TGTTCTTGAAAGCTGCTCAGTGGTTCAAGCTACAGCATGGTGGACTAGCAGAATGGACTCCAGGGCCTC
CGAGGAGACAGTGACTGCTGCCAGAAATAGTCAAGGATAGAAAGGAAGGACTTCACTGAGGC

FLA331651 (S = G/C) (SEQ ID NO: 516)

CGCTTTCGAGCAGATGAGTGTTGTAGATTACAGTGTTGAGAGCTGTTTGTGTCCAGAGCTGCTTGCTGC
ACCTGGCGGGATAAACACTGGTCTAACAGAGGATCCTTGTTTCAAGGAGGCTGCCTTTTATTGGGGGG
ACAAAATTGTTCTTGAAAGCTGCTCAGTGGTTCAAGCTACAGCATGGTGGACTAGCAGAATG

S

ACTCCAGGGCCTCCGAGGAGACAGTGACTGCTGCCAGAAATAGTCAAGGATAGAAAGGAAGGACTTCAC
TGAGGCCTGGGAGAAGATTATGGAATGGGACTGACAGCAGTGACGGGGAGTAAAGGGGGTGTCTGGGG
GAATTGTGCCCCATGGTGAGAGCTAGAGGGTTCAAAAGACTTAACCCGACGCATCTCTCTC

FLA331841 (R = G/A) (SEQ ID NO: 517)

TAGCAGAATGGACTCCAGGGCCTCCGAGGAGACAGTGACTGCTGCCAGAAATAGTCAAGGATAGAAAGG
AAGGACTTCACTGAGGCCTGGGAGAAGATTATGGAATGGGACTGACAGCAGTGACGGGGAGTAAAGGG
GGTGTCTGGGGGAATTGTGCCCCATGGTGAGAGCTAGAGGGTTCAAAAGACTTAACCCGAC

R

CATCTCTCTCACCTGGAGATTGGGCCCCGTTCAATCTAACTGGATGGCTATAATTTAAAAGGTTTAGGT
ATTATGACAAACATGGATATATTAGGTGATAGCAATGCAAAATGCATATGGCTTCTTGATATAAAACAC
AAGACTTGAAAGCAGCATCTTTGGCTGGGTACTACAGCCACCCTCCTCTGTCTACTAAGGGAG

SG13S86 (R= G/A) (SEQ ID NO: 518)

CAGCAACATATCTGTGTGCCTGTCTGGGTTGTAAAAAGGGTCAAAGATCAATGCAGCAGGCAGCTACAT
GCTGGCAAAAGCCAGAGGCAGCTGGTCTGTTTGCCTGTGCCAGGAAACCACTGGGAATGGGGTTGTGTG
TTATTCTAGGAGAAAGTCGTCCAGCAGCAGCTTCTCCAGGGGCATCCAAGAGCACTGAAAA

R

GGTTGCAAGATGACCCATGAGGCTGCAGGAAGAAAAGAACATGCATTTAATCTTGCTATCTGAAAAGTA
AGACATGAAGCTTTCTCTCATTTTTAATATACACATGGACAGTAGTATGTGTATATAGTTTATATGCAA
TATACTTGTTATAAGGTTGCATGCTCAAAATTTTGGTTTATGGGGTGTGGGATCATAAATG

SNP13B_R1028729 (Y=C/T) (SEQ ID NO: 519)

CTACAAAAATTACCATCATATGCTGTCTGTCATGCTGCTGCCAGTCTATTTATCATATTATTTAAGAAACA
AACATTTATTGAAGATTTATCATGTGCTCAGCACTGCCAAAGAGGAAATAAAGAGCATAATATCTATTC
TTAGAAAATAACATTAAACAAATAGAAAACAAGAAACCATAATGTTAAAAATATTACATAG

Y

FIG. 8R

129/132

AACACAGAAAGACAATGTATAATTATACATACGCACTAAAGCAAAGATAACATAATTTATAAATTATGA
GGTACAGAATAGTTAGATTCTGAAAATTAAATAATCAGGAAAACTTCATGAAGATGAGATCTGGGCT
GGATCCCAAAGGATAGGCAGGTGGATCATGTAGAACAGGGGAAAGGAGTTCCTGATCGGGGA

SNP13B_Y1323898 (R=G/A) (SEQ ID NO: 520)
GAACTAAAGAAAGCCACAAAAGTTACCTCAATGCCAAGACATTTCTTGATTTTTGAAAACCCAGTTG
TCGAACCACCCATCTATAGAACTTGAAAGACTAAAACTATCTTACTCTAAACATTTTCTAGGAAGTT
GATTCTACAACACATTTTGGTTTTCCAATTTGGCTTCTAATAATTATTTCAAAGTTTCTGTG

R
CCTAAATTTTGTGTTTACATTGATCCTTTGAATGGACTACTGTTTCCACATTTTAGAACATTTAAAAAGA
TATCTACAACCCGAGTCTAATCATAAAAAAATCAGACAGATCCAAAATGTGGAACATTCCTACTAAAAA
AGGAGTGGGGAGAGGTCTTTATTCTTCCAAAAATATCAATGCCATAAAAGACAAAGACGGCT

SNP13B_K912392 (Y=T/C) (SEQ ID NO: 521)
TGTGGTATGAGGTAAGGATCCATTTTTCCTTTGTCATAGCCAGTTTTGTAGCTCCACTTTATTTT
CTCACTTGATCTGCCATGCCACCTCTAGCATGTATCAACATATCATGTATGTGTGCAGCTGTTCTTAA
CTCTCAATTTTATTCTCTTGGTTACTTTGTCTAACCCAGCACTCATACTTTTTTAAATTATTA

Y
GGCTACCTTGTAGGGCAAGAATCCTCACTTTTATTCAACTTCTTTTGAAGTGTCTTGATGCATATTTT
TCTGATCTTACTTGGCCATATATATTTTGGGGACAGATGTGACATCATACCAAGCTTTCTTTGCTTGAC
ATTGTAGATATTTTCTTATTCAATATGTGCTAAAAATTTTGAGTTTGGTCATACAGTCTTT

SNP13B_R1556428 / DG00AAFQR (R=G/A) (SEQ ID NO: 522)
GAGATTATATCCCACTACCACTGCAGCTCCAGGATCCAGCTTCACAAACATTTGTTGAATGAATGAAT
AAGAAAAGAGGACACCCCCAAAGAGGCTGCAAGGGAAAAAGCTACAAAGACAGAAGCACCAGGAAAAAG
TAGGGTCATGTAAGTCAAAGCAGGAAAAAGTTCCATGGTGGGGTGGTCAGCAGTGTCTAAT

R
CCACGAAGGCACAAAGTAGGATAAAGGTTAAAAATCAGCCTTTGGTTTTGGCAAATATGAAGCTTATCG
GTAGCCTTAGCGAGAACAATTCCATCAGGGAGCAGAAGCTAACTGCAGTGGGTTGAGTCATCAAGCAGG
CATAAGGAAGTAGGGATACCCCATTTATAAGCTACTCTTTCAAGAAGCTCAAATCTGAAGGTT

DG00AAFIV (W=T/A) (SEQ ID NO: 523)
TATAAATGATCATTATGTTTCATATTCACACATACAATAATGTACTCAAGTTTATTGCTAAGGTAATTCA
GAATCTCCTTATTTTGAAGTGTGCATTTGATATACCTGTTTGGGAATAACTAGTTTCTTATCTTTGACA
GAAAATAATTTTGTGTTTGTCTTTTACTAAAAAGCATGGTGAAAAATGGCTCCATTTCTA

W
GAGAGGTAATAAATATCGCAATTTGCTGGGTGTCATTAAAGTAACTCACAAGGGAAAAAATGCAAAT
TGGTATCTGCTGATGGAGTAAATCTCCGCAGAAGTGATGACCTGAAAGGATCAATATATTAAGCCCC
TCCAGCTGGTCATTCCAGATTGCAACAATAAAGCATTAAAGTGTAAACCTCAAGGCAGCT

DG00AAFJT (M=C/A) (SEQ ID NO: 524)
ATCTTCAGAAATTGTAATGATGAAAGAGTGCAAGCTCTCACTTCCCCTTCTGTACAGGGCAGGTTGTG
CAGCTGGAGGCAGAGCAGTCTCTCTGCGGAGCTGAAGCAAAACATGGATCAAGAACTGTAGGCAATG
TTGTCTCTGTTGGCCATCGTCACCTCATCAGCGTGGTCCAGAATGGTAAGGAAAGCCCTTCA

M
TCAGGGAAGAACAGAAGGGGAGATTTTCTTTGATGGTTGTTTGGAAAGTCAGGCTTAAACAATTGTGTCT
GTGTGTGCGCATGCACAAACACTTTTACCTTATCTTTATTTTCTTTTATTTGAATGTATAGGGTT
GTGTGTATTTCTGTGTAAATTTGGGGTTTCTCTCTCTTAGTCTTTCACTTTTGTGGTGATT

DG00AAHII (R=G/A) (SEQ ID NO: 525)
AATTTTGAAGCATTTTTCATATGCAAGTGTATACTTCAGAAAGAGAGAGAGAGAGAGGAAAATTGTCCT
GTTCAAGCTTTGCATTTCCATTATTCCTGCTATTAGTTAAAAACAACAACAACAACAAAAACAAGCAG
GATACCTAGATCTGAAAAGGGAGAATTGTGTAGAGCTGTCTTCTAAAGTCTGAGTTAGG

R
CTGCCTCAGACCACTTTTCATAACTATCTCCAGTGGCTTTGTGTTTTATTTATTTAAGATAGAGAAAAA
AAGAGTAATTACTAAGGGCAGCTGCTGTAGCTTTATGGTGATTACTGAACATTGACATGCTGTACAGTT
TTTGGAACTTTGAGTATTTAATCACTTTGGGATATCTATTTTCCCCCATCTTGAGTGTGGA

DG00AAHID (W=T/A) (SEQ ID NO: 526)
ACAGTTGCTCCTGCTGTGTTTCAAGGAAGGGAGTTTCTGTGGTCCCTTTGAAACCACAGAAGAGCCCCCTCG
TATAGCTCTCAATGGAGGGGCAAAACATTCAAATAACTCAGGAGATAACACAACATTTTGTGTTTTAAC
TGTGAGTTTTTAGGCAATCACAAGATCCAGATGTATGTCCCAAGCCTCTCTTTGCAATTCTA

FIG. 8S

130/132

W

TTAACCTCAATGTTGCAACCATAGACCTACCTTACAGAGTTCAAAAAATATGCAAAACCCTGCCTTT
CTTCTTCTCATACCCCAAAATGCCATTCTGAACATTTCTGTTAGTTAAAAAAGATTTCATGGTGT
TACCAGGCACTGTACACAGTCTGTGTCCCAAGACAAGGAGGTACAGTTCCACATGCGCCCAT

DG00AAHIJ (R=G/A) (SEQ ID NO: 527)

AATCATCTGACTTTAGAGAGTAGACACTTGCTCCATGCATATTGCCTCCAATTCATTCAAGCACT
CCCTGCTCAAGAAGTTCTTTCTTATGTTGAGCTGAAATCTGCAGCCCTATGCGTTTTACCCAGCAGTCC
TGGTGTCTGTCCCTAAAATCACCTTAGACTGTGCTGCTCTTTCTGTGTTTACAGTGTGAGCT

R

TAATATCCCCCTCTTCGGCCTAACGTTTCTGAAGTCCCTTGCCACTGGGTCTCCTCTCCTCTTCTGTG
TTCTTTCTAAGAACACCTATGCAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCCTGAGATCCGGGCAT
CGACTCTGTTAGAATAATCTACGTATGAGTTATTTTTTTGAGAACTATGTGTCAATTGCTGAC

DG00AAHIH (R=G/A) (SEQ ID NO: 528)

TTATGTTGAGCTGAAATCTGCAGCCCTATGCGTTTTTACCCAGCAGTCTGGTGTGTTCCCTAAAATCA
CTTAGACTGTGCTGCTCTTTCTGTGTTTACAGTGTGAGCTGTAATATCCCCCTCTTCGGCCTAACGTT
TCTGAAGTCCCTTGCCACTGGGTCTCCTCTCCTCTTCTGTTCTTTCTAAGAACACCTAT

R

CAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCTGAGATCCGGGCATCGACTCTGTTAGAATAATCTA
CGTATGAGTTATTTTTTTGAGAACTATGTGTCAATTGCTGACTCATATTAACCTCTGTGGTTAACTAAAAT
CTCAAGATCTCTTTATGTTTGTGAGAACTTATTTAACTTCTCTGGCCCTCCGTTTCCCTTC

DG00AAHIE (M=C/A) (SEQ ID NO: 529)

AACACCTATGCAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCTGAGATCCGGGCATCGACTCTGTTA
GAATAATCTACGTATGAGTTATTTTTTTGAGAACTATGTGTCAATTGCTGACTCATATTAACCTCTGTGGT
TAACTAAAATCTCAAGATCTCTTTATGTTTGTGAGAACTTATTTAACTTCTCTGGCCCTC

M

GTTTCCTTCACTGAGCAGTGGAGTGATTGATAACCTCCACCTGTGGTTGCTGAAGGTCTTGACAAGAT
GATATAGTTAAAGTAGCTAGCAGTGCCACGTACGGCGGATGCCTCACAACGGTTTGCAGCCATCTCTC
TATCTGTGTCTTTGTCTCTCTCTCACACTGGTTTTGGCTTACTGTTAGCAGCTAGCCGAGAT

DG00AAHIG (Y=C/T) (SEQ ID NO: 530)

CAAAGAAGGTGTCTTTGATGAGGCAAGGTCAAACTTCTCCCCAGACGAAATCCAAAGAAAGCATTCTCT
ACTATGCTATATCAGTTTGGAAAGAAAACTTCTGCCAGGTGACTGCATTCTCACTGGTCACATTGTGT
TCTTATGGACTCCTCAGCTCAACCAATTTGGAGAAGTTATGGTGCAATTTACCATATCTGG

Y

TAGAAGTTAAGTTTCCAATTTGCTGGCAATGAAGAAGAAATGGAGCAGGCCAGGCTGTGTAGTTTCTGC
CACGTGCCCCCGGGAGTGAACAGCTCTGTTTGTAGAAGCCATGGTGCTTAGACCTGGGCTCGCTAGTT
GCCAGCCTCAAATTTGAGAAGTGCCCTTTGGTTGGTGGCTATGCTGTGTCACTTGGGAAGG

DG00AAHIF (S=G/C) (SEQ ID NO: 531)

CCTGGGAAAACATAAGTAAATCAGACACCCGACGTGTGAGCTAGGTTATAATATGCCAGTGAGCCCTG
GGGACATCTTAGCTTTTCAAGAGTCATGCTGTCCAAGCTGACTGTGGGGCTTCCAGAAGGTGGGGAGAGG
AAATGATGCAATGGCCCATCAGAGGCACTACTTGGGGCTGGGGCCAGAGTGCATGTCTAAG

S

CATTAAGGGGAGGGGAGAGCAGCCTTCAATAATTATGAAGAGGAGTCTCAGGTGCACAGCTTCTGATGAG
GGACAGCTTCTAATTGAAGACAGCATTGTGTAATGCTCAAACTCCCTGTCTTCAAGTGCCTGCTGTAT
CCCACCATCAGTTCTGTGACTTCTCCCTAAGCCTCAATTTTGCATGTGTTACATTGGGATAA

DG00AAHOI (R=G/A) (SEQ ID NO: 532)

GGAGAACATGATTAGCATATTTTTTTTAAAGTGAACCTTTAGACCCTTTTTTAAAGGCCTATCTGATTAGG
CCAGGCCCAAGTGAGCTTTAAGTCAACTGATTAGAGATCTTAATTACATCTGCAAAGTCCCTTCATGTT
TACCGTATAACATAACTTAGTGAAAGGAGTGAAATTGCAACCAGGTTCTGCCTGCACTCCAC

R

GAAGGGGATTCTGCAGAAGTGTGGGTACCGGGGGGTTATTTTTGGGATTCTGCCTACGTCACTGAGTCA
AAAGAAGCTGAATGGTTGTGATGCTGAGGTTTTTGGGCAGCAGCAGTGTGTGTGTGTGAGTGAATTCAT
ACGTATGACCACCTGGGAAGAAAGGAGGCTGTGGTTTCTCCACCTCCTGGCAGACAGAGAA

SG13S35 / FLA324333 (R = G/A) (SEQ ID NO: 533)

FIG. 8T

131/132

AGTGCTCTCTAAAGAGCAGTGCTCTACCATCCAAGCTGGGCTTTTCTTTCTTCTTGCTGATAGGGAAG
GCATGGGACATTGCAGGATGGAAGTGGCCCCCAGGCCTTCTCATGCCTGGGCTTGGTTTGGAAAGTGGT
CAGGTGATCAATAATCCTGATTGGCCTGGCATTGAGGAGTTTTCTGGGATGTGGTCCTTTC

R

GTTTTTTAAAAATTATTTTTATTGATACACATATTTGTAGGTATTTGTGGGGTGCATGTGATACTTTAT
TATGTGTGTGGATTGTGTAATGATGAAGTCAGGGCATTAGGGTCTTCATCACCTTGATTATCATTCT
ATGTGTTGAGAACATTTCAAGTTCTCAGTTCCAGCTATTTTGAAATAGACAGTCCATTTTGT

DG00AAFIU / SNP_13_Y1323892 (Y=C/T) (SEQ ID NO: 534)

CTTCTTTTGGCCTGCCTTTCTTCCCTTTCTGTCCTTTTAATTTGCGGGCTTTTGGCAACCACAGCACGGG
TCTGGTTTCTTAGGAGTTTCTTGTAGGATCAAACCGCTAGTTGGCTCTTGGCCCTGTGATAGGGCCC
TGGGCTAACTTATTGGGAAAATGTTGCTGTAACCCCTGCCCAGAGGTGCCTGTGACATGGGC

Y

GCCATCTTCTCCTCTTCCCTTGGCTTCAGCCCCACCTAGAAACCTGAACAAACATTTTCTTGACATTT
CATAAAGTGTGAGTGGCTCCTCATTTAGCAAAATACATCCAGGGAAGTTCAAAAGTGAAAAAGGCCG
TAACTTCTTCTTCTCAGGGACCTACAGAAAATATGTGGCACCTCGGCAGCCTGGCCTGC

DG00AAJFF / FLA287889 (R = G/A) (SEQ ID NO: 535)

GTGCAGTGGCGTGATCCCAGCTCACTGCAATCTCTGCCTCCTGGGTTCAAGTGATTCTCCTGCCTCAGC
CTCCCGAGGGGCTGGGATTGTAGGCGTGACCACTATGCCCATCTAATTTTGTATTTTAGTAGAGAT
AGGGTTTTGCCATTTTGGCCAGACTGTCTTGAACCTCCTGACCTCAGGTGATCTGCCTGCCTC

R

GCCTCCACAGTTTTGTGATTATAGGCATGAGCCACCGTGCCCGGCCTTAACCTTTGTTTTCTTACACA
ACACACTACGTGATGTTTTCCACATGCATGGGTCAATTGCTTCATTACGTACAAATGCATAAGCAATA
TACTGTGTGGTGTGAGTTTGTGATGGGAAAAGGAAGAAGTTTTGCGGATACTACACTGGCTT

FIG. 8U

132/132

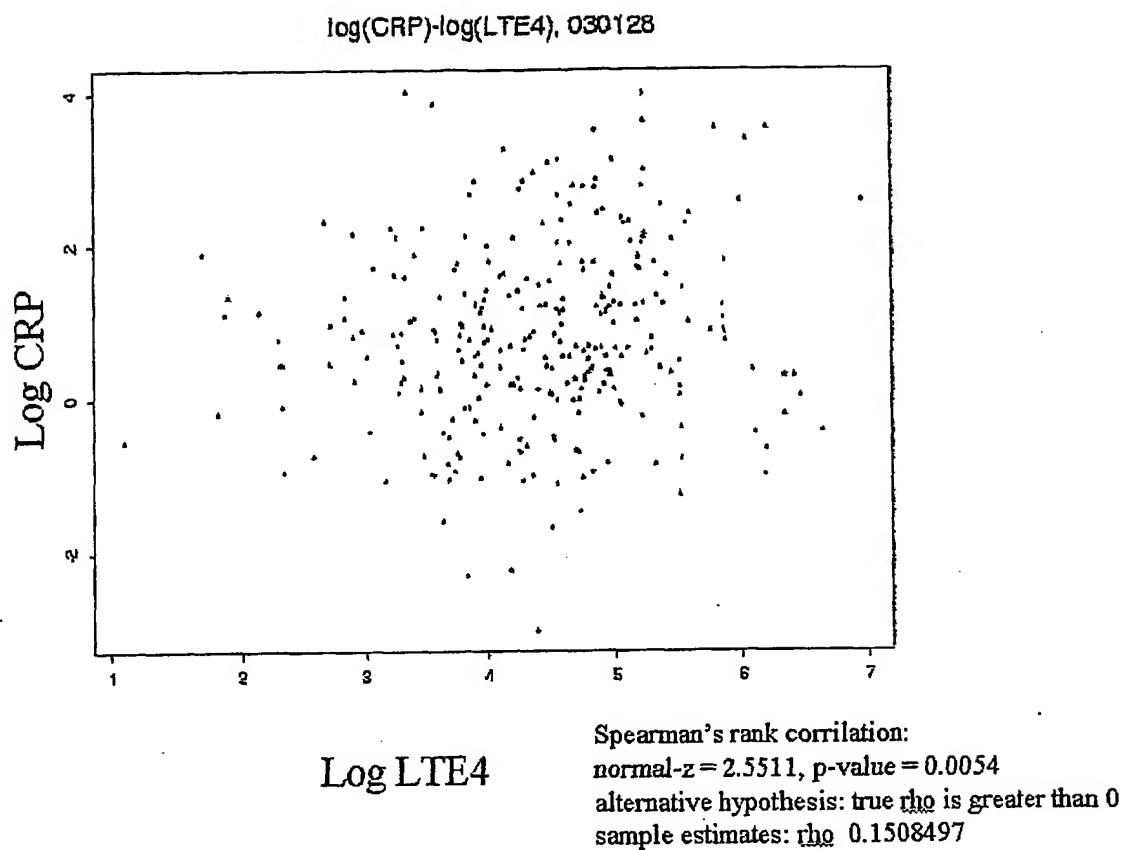


FIG. 9

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(71) Applicant (for all designated States except US): **DECODE GENETICS EHF**. [IS/IS]; Sturlugotu 8, IS-101 Reykjavik (IS).

(72) Inventors; and

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(74) Agent: **GASS, David, A.**; Marshall, Gerstein & Borun LLP, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606-6357 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: SUSCEPTIBILITY GENE FOR MYOCARDIAL INFARCTION; METHODS OF TREATMENT

(57) Abstract: Linkage of myocardial infarction (MI) and a locus on chromosome 13q12 is disclosed. In particular, the FLAP gene within this locus is shown by genetic association analysis to be a susceptibility gene for MI. Pathway targeting for treatment and diagnostic applications in identifying those have MI or at risk of developing MI, in particular are described.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/32556

A. CLASSIFICATION OF SUBJECT MATTER		
IPC(7) : C12Q 1/68; G01N 33/53; A61K 38/17; C07H 21/04; C07K 14/435		
US CL : 435/6, 7.1; 514/2; 536/23.2, 23.5; 530/350		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/6, 7.1; 514/2; 536/23.2, 23.5; 530/350		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) Please See Continuation Sheet		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X — Y	US 5,641,789 A (MARFAT) 24 June 1997 (24.06.1997), see entire reference, particularly column 1, lines 10-21.	1,3,7,19,22,26,38,40, 44,56,59,63,75,78,82, 94-95 2,4-6,8-18,20-21,23- 25,27-37,39,41-43,45- 55,57-58,60-62,64- 74,76-77,79-81,83- 93,96-128
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
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Date of the actual completion of the international search		Date of mailing of the international search report
30 September 2004 (30.09.2004)		21 OCT 2004
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703) 305-3230		Authorized officer Diana B. Johansen Telephone No. 571/272-1600

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INTERNATIONAL SEARCH REPORT

PCT/US03/32556

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X -- Y	US 6,166,031 A (EGGLER et al) 26 December 2000 (26.12.2000), see entire reference, particularly column 13, lines 9-33.	1,3,7,19,22,26,38,40 ,44,56,59,63,75,78,8 2,94-95 2,4-6,8-18,20-21,23- 25,27-37,39,41- 43,45-55,57-58,60- 62,64-74,76-77,79- 81,83-93,96-128
A	FOLCO et al. Leukotrienes in cardiovascular diseases. American Journal of Respiratory and Critical Care Medicine. February 2000, Vol. 161, No. 2, pages S112-S116, see entire reference.	1-128

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INTERNATIONAL SEARCH REPORT

PCT/US03/32556

Continuation of B. FIELDS SEARCHED Item 3:

USPT, DWPI, PGPB, Medline, Lifesci, Scisearch, Embase, Biosis, Caplus

search terms: leukotriene, inhibit####, treat####, myocardial infarction, cardiac arrest, acute coronary syndrome, atherosclerosis;
inventors' names

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